

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2003, 09:50:12 ; Search time 23 Seconds
(Without alignments)

2119,892 Million cell updates/sec

Title: US-09-977-261-2

Perfect score: 2671

Sequence: 1 MAGRGLVSWRAFGCDSEAE.....PASVSGDADGSTRSPRSEP 507

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|---------------------------|
| 1 | 2671 | 100.0 | 507 | 2 | A55625 protein-tyrosine k |
| 2 | 2445 | 91.5 | 527 | 2 | A49865 protein-tyrosine k |
| 3 | 2341 | 87.6 | 505 | 2 | I59286 protein-tyrosine k |
| 4 | 2221.5 | 83.2 | 467 | 2 | I56579 protein-tyrosine k |
| 5 | 2209.5 | 82.7 | 465 | 2 | I48926 protein-tyrosine k |
| 6 | 1253.5 | 46.9 | 450 | 2 | I41973 protein-tyrosine k |
| 7 | 1245.5 | 46.6 | 450 | 1 | JH0559 protein-tyrosine k |
| 8 | 1242.5 | 46.5 | 450 | 1 | S15094 protein-tyrosine k |
| 9 | 1227.5 | 46.0 | 450 | 2 | I48929 protein-tyrosine k |
| 10 | 762.5 | 28.5 | 507 | 2 | A39939 protein-tyrosine k |
| 11 | 751.5 | 28.1 | 509 | 1 | I48845 protein-tyrosine k |
| 12 | 742.5 | 27.8 | 509 | 1 | OKH0UK protein-tyrosine k |
| 13 | 736 | 27.6 | 545 | 2 | S52313 protein-tyrosine k |
| 14 | 735 | 27.5 | 533 | 1 | TVCHS protein-tyrosine k |
| 15 | 734.5 | 27.5 | 526 | 1 | TVFV60 protein-tyrosine k |
| 16 | 734 | 27.5 | 568 | 1 | TVFVS1 protein-tyrosine k |
| 17 | 734 | 27.5 | 557 | 1 | TVFVS2 protein-tyrosine k |
| 18 | 733 | 27.4 | 546 | 2 | S52314 protein-tyrosine k |
| 19 | 731.5 | 27.4 | 587 | 1 | TVFVPR protein-tyrosine k |
| 20 | 730.5 | 27.3 | 526 | 2 | S20808 protein-tyrosine k |
| 21 | 730.5 | 27.3 | 526 | 2 | S26420 protein-tyrosine k |
| 22 | 727.5 | 27.2 | 523 | 1 | TVFVMT protein-tyrosine k |
| 23 | 724.5 | 27.1 | 532 | 1 | OKFYVR protein-tyrosine k |
| 24 | 724 | 27.1 | 532 | 1 | A34104 protein-tyrosine k |
| 25 | 724 | 27.1 | 532 | 1 | B34104 protein-tyrosine k |
| 26 | 724 | 27.1 | 1520 | 1 | TVFVFA protein-tyrosine k |
| 27 | 723.5 | 27.1 | 526 | 1 | TVFVR protein-tyrosine k |
| 28 | 720.5 | 27.0 | 505 | 1 | TVH0UC protein-tyrosine k |
| 29 | 718 | 26.9 | 542 | 1 | TVH0UC protein-tyrosine k |

| | | | | | |
|----|-------|------|-----|---|---------------------------|
| 30 | 716.5 | 26.8 | 526 | 2 | S15582 protein-tyrosine k |
| 31 | 716 | 26.8 | 505 | 1 | S24550 protein-tyrosine k |
| 32 | 714 | 26.7 | 541 | 1 | A43610 protein-tyrosine k |
| 33 | 713 | 26.7 | 506 | 1 | S24553 protein-tyrosine k |
| 34 | 713 | 26.7 | 512 | 1 | I56160 protein-tyrosine k |
| 35 | 713 | 26.7 | 528 | 1 | TVFVCG protein-tyrosine k |
| 36 | 710 | 26.6 | 541 | 2 | S31645 protein-tyrosine k |
| 37 | 710 | 26.6 | 543 | 1 | TVH0VS protein-tyrosine k |
| 38 | 709 | 26.5 | 537 | 2 | I51592 protein-tyrosine k |
| 39 | 707 | 26.5 | 512 | 1 | TVH0LX protein-tyrosine k |
| 40 | 706 | 26.4 | 541 | 1 | TVCHS protein-tyrosine k |
| 41 | 706 | 26.4 | 542 | 2 | A49114 protein-tyrosine k |
| 42 | 705 | 26.4 | 544 | 2 | I51593 protein-tyrosine k |
| 43 | 701 | 26.2 | 512 | 1 | A39719 protein-tyrosine k |
| 44 | 700.5 | 26.2 | 503 | 1 | J01371 protein-tyrosine k |
| 45 | 699.5 | 26.2 | 536 | 2 | S33569 protein-tyrosine k |

ALIGNMENTS

RESULT 1
A55625
protein-tyrosine kinase (EC 2.7.1.112) matk, short splice form - human
N:Alternate names: hematopoietic consensus tyrosine-lacking (HYL) non-receptor tyrosi
C:Species: Homo sapiens (man)
C>Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 26-May-2000
C:Accession: A55625; S43533; I58397; T46323
J:Avraham, S.; Jiang, S.; Oka, S.; Fu, Y.; Deng, B.; Dowler, L.L.; White, R.A.; Avrah
J. Biol. Chem. 270, 1833-1842, 1995
A:Title: Structural and functional studies of the intracellular tyrosine kinase MATK
A:Reference number: A55625; MUID:95130565; PMID:7530249
A:Accession: A55625
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-507 <AVR>
A:Cross-references: GB:S75164; NID:9896217; PIDN:MAC60645.1; PID:9896220
R:Sakano, S.; Iwama, A.; Imazawa, J.; Ariyama, T.; Ohno, M.; Suda, T.
Oncogene 9, 1155-1161, 1994
A:Title: Molecular cloning of a novel non-receptor tyrosine kinase, HYL (hematopoietic
A:Reference number: S43533; MUID:94181267; PMID:8134117
A:Accession: S43533
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-507 <SAK>
A:Cross-references: EMBL:X77278; NID:9471312; PIDN:CA54493.1; PID:9557272
R:McVicar, D.W.; Lal, B.K.; Lloyd, A.; Kawamura, M.; Chen, Y.Q.; Zhang, X.; Staples,
Oncogene 9, 2037-2044, 1994
A:Title: Molecular cloning of Isk, a carboxyl-terminal src kinase (csk) related gene,
A:Reference number: I58397; MUID:94268844; PMID:7516063
A:Accession: I58397
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 42-149, 'GG', 152-160, 'T', 162-258, 'C', 261-296, 'D', 298-336, 'R', 338-362, 'E', 3
A:Cross-references: GB:S71669; NID:9559593; PIDN:AAB30995.1; PID:9559594
R:Duesterhoefl, A.; Lauber, J.; Mewes, H.W.; Well, B.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A:Reference number: Z23036
A:Accession: T46323
A:Molecule type: mRNA
A:Residues: 1-507 <AAA>
A:Cross-references: EMBL:AL137754
A:Experimental source: adult testis; clone DKFZp434N1212
C:Comment: For an alternative splice form, see FIR:A4965.
C:Gene: GDB:MATK; Isk
A:Cross-references: GDB:304667
A:Map position: 19p13.3-19p13.3
A>Note: DKFZp434N1212.1
C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH
C:Keywords: alternative splicing; ATP; phosphotransferase; tyrosine-specific protein
F:55-105/Domain: SH3 homology <SH3>
F:122-211/Domain: SH2 homology <SH2>

F:233-485/Domain: protein kinase homology <KIN>
F:241-249/Region: protein kinase ATP-binding motif

Query Match 100.0%; Score 2671; DB 2; Length 507;
Best Local Similarity 100.0%; Pred. No. 4.5e-130;
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MAGRGLSVRAHFGCDASAEELPRVSPRFLRAWHPPVSAARMPTRRAPPTQCTTCKEHT 60
DB 1 MAGRGLSVRAHFGCDASAEELPRVSPRFLRAWHPPVSAARMPTRRAPPTQCTTCKEHT 60
QY 61 RPRPGEIAFRKGDVYITLLECEKNSWYRVKHNHTSGOGLLAAGALREALSDPKLSLM 120
DB 61 RPRPGEIAFRKGDVYITLLECEKNSWYRVKHNHTSGOGLLAAGALREALSDPKLSLM 120
QY 121 PMFHGKISGGEAVOQLOPPEDGLFLVRESARHPGDVYLCVSPGSDVYHRYVLRDGLTI 180
DB 121 PMFHGKISGGEAVOQLOPPEDGLFLVRESARHPGDVYLCVSPGSDVYHRYVLRDGLTI 180
QY 181 DEAVFECNLMADMEYHSKDKGAICTKLVPRKRKHGKTSABEELARAGWMLNLOHLLTGAQ 240
DB 181 DEAVFECNLMADMEYHSKDKGAICTKLVPRKRKHGKTSABEELARAGWMLNLOHLLTGAQ 240
QY 241 IGGERGAVYQGEYLGOKVAVKNIKCDVTAQAFLEDAVMTKMOHENLVRLGLVILHOG 300
DB 241 IGGERGAVYQGEYLGOKVAVKNIKCDVTAQAFLEDAVMTKMOHENLVRLGLVILHOG 300
QY 301 YIYMEHYSKGNLVNFLTREGALVNTAQLQFSLHVAEGMEYLESKKLVHRDLAARNILV 360
DB 301 YIYMEHYSKGNLVNFLTREGALVNTAQLQFSLHVAEGMEYLESKKLVHRDLAARNILV 360
QY 361 SEDLVAKVSPFGIAKAKRKLDSSRLPVKWTAPALAKHGFTSKSDVWSGVLMEVFSY 420
DB 361 SEDLVAKVSPFGIAKAKRKLDSSRLPVKWTAPALAKHGFTSKSDVWSGVLMEVFSY 420
QY 421 GRAPYPRMSLKEYSEAVEKEGYRMEPEGCGPVHVLMSGWEAPARPPFRKLAEKLAR 480
DB 421 GRAPYPRMSLKEYSEAVEKEGYRMEPEGCGPVHVLMSGWEAPARPPFRKLAEKLAR 480
QY 481 ELRSAGAPASVSGODADGSTSPRSQEP 507
DB 481 ELRSAGAPASVSGODADGSTSPRSQEP 507

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RESULT 2

A:9865
protein-tyrosine kinase (EC 2.7.1.112) matk, long splice form - human
N:Alternate names: hematopoietic consensus tyrosine-lacking (HVL) non-receptor tyrosine
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1995 #sequence_revision 30-Jun-1995 #text_change 26-May-2000
C:Accession: A49865
R:Benabib, B.D.; Cowley, S.; Jiang, S.; London, R.; Deng, B.; Grabarek, J.; Groopman, J.
J. Biol. Chem. 269, 1068-1074, 1994
A:Title: Identification and characterization of a novel tyrosine kinase from megakaryocytes
A:Reference number: A49865; MUID:94117408; PMID:8288563
A:Accession: A49865
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-527 <BEN>
A:Cross-references: GB:L18974; NID:9455449; PIDN:AAA16703.1; PID:9459550
C:Comment: For an alternative splice form, see PIR:A55625.
C:Genetics:
A:Gene: GDB:MATK, 1sk
A:Cross-references: GDB:304667
A:Map position: 19p13.3-19p13.3
A:Note: DKFZP434N1212.1
C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology; SH3 domain; SH3 homology <SH2>
C:Keywords: alternative splicing; ATP; phosphotransferase; tyrosine-specific protein kin
F:122-211/Domain: SH2 homology <SH2>
F:233-484/Domain: protein kinase homology <KIN>
F:241-249/Region: protein kinase ATP-binding motif

Query Match 91.5%; Score 2445; DB 2; Length 527;
Best Local Similarity 93.5%; Pred. No. 1.8e-118;
Matches 472; Conservative 1; Mismatches 18; Indels 14; Gaps 2;

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QY 1 MAGRGLSVRAHFGCDASAEELPRVSPRFLRAWHPPVSAARMPTRRAPPTQCTTCKEHT 60
DB 1 MAGRGLSVRAHFGCDASAEELPRVSPRFLRAWHPPVSAARMPTRRAPPTQCTTCKEHT 60
QY 61 RPRPGEIAFRKGDVYITLLECEKNSWYRVKHNHTSGOGLLAAGALREALSDPKLSLM 120
DB 61 RPRPGEIAFRKGDVYITLLECEKNSWYRVKHNHTSGOGLLAAGALREALSDPKLSLM 120
QY 121 PMFHGKISGGEAVOQLOPPEDGLFLVRESARHPGDVYLCVSPGSDVYHRYVLRDGLTI 180
DB 121 PMFHGKISGGEAVOQLOPPEDGLFLVRESARHPGDVYLCVSPGSDVYHRYVLRDGLTI 180
QY 181 DEAVFECNLMADMEYHSKDKGAICTKLVPRKRKHGKTSABEELARAGWMLNLOHLLTGAQ 240
DB 181 DEAVFECNLMADMEYHSKDKGAICTKLVPRKRKHGKTSABEELARAGWMLNLOHLLTGAQ 240
QY 241 IGGERGAVYQGEYLGOKVAVKNIKCDVTAQAFLEDAVMTKMOHENLVRLGLVILHOG 300
DB 241 IGGERGAVYQGEYLGOKVAVKNIKCDVTAQAFLEDAVMTKMOHENLVRLGLVILHOG 300
QY 301 YIYMEHYSKGNLVNFLTREGALVNTAQLQFSLHVAEGMEYLESKKLVHRDLAARNILV 360
DB 301 YIYMEHYSKGNLVNFLTREGALVNTAQLQFSLHVAEGMEYLESKKLVHRDLAARNILV 360
QY 361 SEDLVAKVSPFGIAKAKRKLDSSRLPVKWTAPALAKHGFTSKSDVWSGVLMEVFSY 420
DB 361 SEDLVAKVSPFGIAKAKRKLDSSRLPVKWTAPALAKHGFTSKSDVWSGVLMEVFSY 419
QY 421 GRAPYPRMSLKEYSEAVEKEGYRMEPEGCGPVHVLMSGWEAPARPPFRKLAEKLAR 480
DB 420 GRAPYPRMSLKEYSEAVEKEGYRMEPEGCGPVHVLMSGWEAPARPPFRKLAEKLAR 469
QY 481 ELRSAGAPASVSGODADGSTSPRSQ 505
DB 470 ---SAMPWRSPGSAVAVQVPPSPQ 491

```

RESULT 3

I59296
protein-tyrosine kinase (EC 2.7.1.112), megakaryocyte-associated - mouse
N:Alternate names: Mus musculus (house mouse)
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 04-Feb-2000
C:Accession: I59296; I58407; B55625; I49621
R:Chow, L.M.L.; Jarvis, C.D.; Hu, Q.; Nye, S.H.; Gervais, F.G.; Veillette, A.; Matis, Proc. Natl. Acad. Sci. U.S.A. 91, 4975-4979, 1994
A:Title: Ntk: A Csk-related protein-tyrosine kinase expressed in brain and T lymphocytes
A:Reference number: I59296; MUID:94255451; PMID:8197166
A:Accession: I59296
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-505 <RES>
A:Cross-references: GB:L27738; NID:9507289; PIDN:AAB59677.1; PID:9507290
R:Chow, L.M.; Davidson, D.; Fournel, M.; Gosselin, P.; Lemieux, S.; Lyu, M.S.; Kozak, Oncogene 9, 3437-3448, 1994
A:Title: Two distinct protein isoforms are encoded by ntk, a csk-related tyrosine protein kinase
A:Reference number: I58407; MUID:95060800; PMID:7970703
A:Accession: I58407
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-43 <RE2>
A:Cross-references: GB:I33339; NID:9609536; PIDN:AAA64431.1; PID:9609537
R:Avraham, S.; Jiang, S.; Ota, S.; Fu, Y.; Deng, B.; Dowler, L.L.; White, R.A.; Avraham, J. Biol. Chem. 270, 1833-1842, 1995
A:Title: Structural and functional studies of the intracellular tyrosine kinase MATK
A:Reference number: A55625; MUID:95130565; PMID:7530249
A:Accession: B55625
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA

R:Garvin, A.M.; Pawar, S.; March, J.D.; Perlmutter, R.M.
 Mol. Cell. Biol. 8, 3058-3064, 1988
 A:Title: Structure of the murine lck gene and its rearrangement in a murine lymphoma cell
 A:Reference number: 157636; MUID:89096891; PMID:2850479
 A:Accession: 177452
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-35, 'VR' <GRR>
 A:Cross-references: GB:M2151; NID:g18768; PIDN:AAA9422.1; PID:g554186
 C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3
 C:Keywords: ATP; autophosphorylation; blocked amino end; kinase-related transforming pr
 F:68-116/Domain: SH3 homology <SH3>
 F:127-224/Domain: SH2 homology <SH2>
 F:243-501/Domain: protein kinase homology <KIN>
 F:251-259/Region: protein kinase ATP-binding motif
 F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F:273/Active site: Lys #status predicted
 F:394,505/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 28.1%; Score 751.5; DB 1; Length 509;
 Best Local Similarity 38.3%; Pred. No. 1,le-31;
 Matches 164; Conservative 84; Mismatches 155; Indels 25; Gaps 9;
 Oy 65 GELAFRRGDVVTILEACENKSWYRKHTSGQEGLLAAGALRREALSADPKLSMPWFH 124
 Db 78 GDLGFEKGEOLRIE--QSGEMWKAOSLTGQEGFIFENFAKANSLEPE-----PWEE 129
 Oy 125 GKIGQAVQOOLQPED--GLFLVRESARHGDVLYV-----SFGDVIHYRLHND-G 176
 Db 130 KNLSRKAERQLAPGHTHSEFLRESESTAGSFLVRPDQNGEVVKKYKIRNDNG 189
 Oy 177 HLTFIDEAVFCNLDMNEVHSKDKAICTKLVPRKRGKTSAREELARAGMLNLQHLT 236
 Db 190 GFYSPIRTPRGHLDVLRHTNADSGICTKLSRQC---IQKPKPMWEDMEVPRRELK 246
 Oy 237 LGAOIGGEGAVLQGEYLQ--KVAVKNIK--CDVTAQFLDETVMTKMOENLVRLGV 294
 Db 247 LVEFLGAGGEGEVMGNGYNGHTKVAVSLKOGSMSPALFAEAMIMOLQHPRLVRYAV 306
 Oy 295 ILHGLTYMEVSKGNLVNLFRTGRALVNTAQLQFLSHVAGLESEKLVHDLA 354
 Db 307 VTQPIITITTYEMKNGSLVDFLTKPSGKILNVKLLDMAOIAAGMAFIEQNTYHDLR 366
 Oy 355 ARNLIVSEDLVAVKVDGLAKA---ERKGLDSSRLPVKTAPEALKHGKTSKDVWSF 410
 Db 367 AANILVSDTLSCRIADGLARLIEDNETYAREGAKPKIKMTAPALINVGFTIKSDVWSF 426
 Oy 411 GVLLMEVSTGRAPYPMKSLKEVSEAVEKGYRMEPECCPGPVHVLSSCWAEAPRRP 470
 Db 427 GILTEIVTGRIRIYPGMPNTPEYIQLNERYGRVVRPNCPBELYHMLCWEKRPEDRPT 486
 Oy 471 FRKLAETL 478
 Db 487 FDYLRVYL 494

RESULT 12

OKHUK

protein-tyrosine kinase (EC 2.7.1.112) lck - human
 N:Alternate names: kinase-related transforming protein (lck)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1992 #sequence,revision 30-Sep-1992 #text,change 28-Jan-2000
 C:Accession: J00152; S07822; S07823; S07143; A32797; I57636
 R:Rouyer, E.; Van Huynh, T.; de Souza, S.L.; Lang, M.C.; Fischer, S.; Benarous, R.
 Gene 84, 105-113, 1989

A:Title: Structure of the human lck gene: differences in genomic organisation within src
 A:Reference number: J00152; MUID:90108697; PMID:2558056
 A:Accession: J00152
 A:Molecule type: DNA
 A:Residues: 1-509 <ROU>
 A:Cross-references: EMBL:X14053
 R:Perlmutter, R.M.; March, J.D.; Lewis, D.B.; Peet, R.; Ziegler, S.F.; Wilson, C.B.
 J. Cell. Biochem. 38, 117-126, 1988

A:Title: Structure and expression of lck transcripts in human lymphoid cells.
 A:Reference number: S07822; MUID:89123626; PMID:3265417
 A:Accession: S07822
 A:Molecule type: mRNA
 A:Residues: 1-86, 'P', '88-509' <PER>
 A:Cross-references: EMBL:X1529; NID:g34294; PIDN:CAA3184.1; PID:g34295
 R:Koga, Y.; Caccia, N.; Toyonaga, B.; Spolski, R.; Yanagi, Y.; Yoshikata, Y.; Mak, T.W
 Eur. J. Immunol. 16, 1643-1646, 1986
 A:Title: A human T cell-specific cDNA clone (YT16) encodes a protein with extensive h
 A:Reference number: S07200; MUID:87133831; PMID:3493153
 A:Accession: S07200
 A:Molecule type: mRNA
 A:Residues: 1-205, 'ASAIPPT', '212-257', 'RCGW', '262', 'TTT', '266', 'T', '268-281', 'AGRLP', '287-503',
 A:Cross-references: EMBL:X05027; NID:g36807; PIDN:CAA28691.1; PID:g36808
 R:Velluthe, A.; Foss, F.M.; Sauvillie, E.A.; Bolen, J.B.; Rosen, N.
 Oncogene Res. 1, 357-374, 1987
 A:Title: Expression of the lck tyrosine kinase gene in human colon carcinoma and othe
 A:Reference number: S01879; MUID:88217332; PMID:2835736
 A:Accession: S01879
 A:Molecule type: mRNA
 A:Residues: 368-471, 'H', '473-509' <VER>
 A:Cross-references: EMBL:X06369; NID:g34288; PIDN:CAA29667.1; PID:g34289
 R:Trevillian, J.M.; Lin, Y.; Chen, S.J.; Phillips, C.A.; Canna, C.; Linna, T.J.
 Biochim. Biophys. Acta 888, 286-295, 1986
 A:Title: Human T lymphocytes express a protein-tyrosine kinase homologous to p56(LSTR
 A:Reference number: S07143; MUID:87000726; PMID:3489486
 A:Accession: S07143
 A:Molecule type: mRNA
 A:Residues: 'A', '376-509' <TR>
 A:Cross-references: EMBL:X04476; NID:g35779; PIDN:CAA28165.1; PID:g35780
 R:Takadera, T.; Leung, S.; Gerone, A.; Koga, Y.; Takihara, Y.; Miyamoto, N.G.; Mak,
 Mol. Cell. Biol. 9, 2173-2180, 1989
 A:Title: Structure of the two promoters of the human lck gene: differential accumulat
 A:Reference number: A32797; MUID:89313764; PMID:2787474
 A:Accession: A32797
 A:Molecule type: DNA
 A:Residues: 1-35 <TAK>
 A:Cross-references: GB:M26692; NID:g341523; PIDN:AAA59503.1; PID:g349702
 R:Garvin, A.M.; Pawar, S.; March, J.D.; Perlmutter, R.M.
 Mol. Cell. Biol. 8, 3058-3064, 1988
 A:Title: Structure of the murine lck gene and its rearrangement in a murine lymphoma
 A:Reference number: 157636; MUID:89096891; PMID:2850479
 A:Accession: 157636
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-35, 'VR' <RR>
 A:Cross-references: GB:M21510; NID:g187031; PIDN:AAA59501.1; PID:g553522
 C:Comment: Protein tyrosine kinases play important roles in the control of cell growt
 C:Genetics:
 A:Gene: GDB:ICK
 A:Cross-references: GDB:119360; OMIM:153390
 A:Map position: 1p35-1p34.3
 A:Introns: 35/3; 63/1; 93/2; 126/2; 161/1; 211/1; 262/1; 322/1; 347/3; 399/1; 443/1
 C:Function:
 A:Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
 C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH
 C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation;
 F:2-509/Product: protein-tyrosine kinase lck #status predicted <MAT>
 F:68-116/Domain: SH3 homology <SH3>
 F:127-224/Domain: SH2 homology <SH2>
 F:243-501/Domain: protein kinase homology <KIN>
 F:251-259/Region: protein kinase ATP-binding motif
 F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F:3,5/Binding site: palmitate (Cys) (covalent) #status predicted
 F:273/Active site: Lys #status predicted
 F:394,505/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status p

Query Match 27.8%; Score 742.5; DB 1; Length 509;
 Best Local Similarity 37.6%; Pred. No. 3,2e-31;
 Matches 161; Conservative 87; Mismatches 155; Indels 25; Gaps 9;
 Oy 65 GELAFRRGDVVTILEACENKSWYRKHTSGQEGLLAAGALRREALSADPKLSMPWFH 124
 Db 78 GDLGFEKGEOLRIE--QSGEMWKAOSLTGQEGFIFENFAKANSLEPE-----PWEE 129
 Oy 125 GKIGQAVQOOLQPED--GLFLVRESARHGDVLYV-----SFGDVIHYRLHND-G 176
 Db 130 KNLSRKAERQLAPGHTHSEFLRESESTAGSFLVRPDQNGEVVKKYKIRNDNG 189
 Oy 177 HLTFIDEAVFCNLDMNEVHSKDKAICTKLVPRKRGKTSAREELARAGMLNLQHLT 236
 Db 190 GFYSPIRTPRGHLDVLRHTNADSGICTKLSRQC---IQKPKPMWEDMEVPRRELK 246
 Oy 237 LGAOIGGEGAVLQGEYLQ--KVAVKNIK--CDVTAQFLDETVMTKMOENLVRLGV 294
 Db 247 LVEFLGAGGEGEVMGNGYNGHTKVAVSLKOGSMSPALFAEAMIMOLQHPRLVRYAV 306
 Oy 295 ILHGLTYMEVSKGNLVNLFRTGRALVNTAQLQFLSHVAGLESEKLVHDLA 354
 Db 307 VTQPIITITTYEMKNGSLVDFLTKPSGKILNVKLLDMAOIAAGMAFIEQNTYHDLR 366
 Oy 355 ARNLIVSEDLVAVKVDGLAKA---ERKGLDSSRLPVKTAPEALKHGKTSKDVWSF 410
 Db 367 AANILVSDTLSCRIADGLARLIEDNETYAREGAKPKIKMTAPALINVGFTIKSDVWSF 426
 Oy 411 GVLLMEVSTGRAPYPMKSLKEVSEAVEKGYRMEPECCPGPVHVLSSCWAEAPRRP 470
 Db 427 GILTEIVTGRIRIYPGMPNTPEYIQLNERYGRVVRPNCPBELYHMLCWEKRPEDRPT 486
 Oy 471 FRKLAETL 478
 Db 487 FDYLRVYL 494

Db 78 GDGFEKGEQRLILE--QSGEMWKAQSLTTGEGFIPFNFAKANSLPE-----PWF2 129
 QY 125 GKISGEAVOOLQPPED--GLFLVRESARHPGDYLCV-----SFGDVIHYHVLHND-G 176
 Db 130 KNISKRDAERQQLAPGNTGHSFLIRESESTAGSFSLSVRPFDQOGEVVAHVIYRLNDNG 189
 QY 177 HLTIIDEAVFCNLMDEVHNSKDKGAICTKLVRPKRKHGKSAEELARAGWLLNLQHLT 236
 Db 190 GFYISPRITFPGLHELVRYHTNNSDGLCTRLSRPCQ---TQKPKQWMEDEWEVPRFTLK 246
 QY 237 LGAOIGERGAVLQGEYLQ--KVAYKNIK-CDVTAQAFIDEFAVMTKMOHENLVRLGCV 294
 Db 247 LVERLAGOGEVWMEGYNHTVAVKSLQSGMSPDPAFLAEANLMOQLHQRVRLYAV 306
 QY 295 ILHGLYIVMEHNSKGLVNFELTRGRALVNTAQLLOFSLHVAEGMEYLESKLVHNDLA 354
 Db 307 VTQEPITITFEVWENSLVDFLKTSPGSKITKLTKLMDMAQIABGAFAIERKNYIHRDLK 366
 QY 355 ANNLVSEDLVAVVSDFGAKA---ERKGLDSSRLPVKWTAPDALKHGFTSKSDVWSF 410
 Db 367 AANILVSDTLSCIKIADFGIARLTIEDNEYTAREGAKFPKWTAPDALINYGFTIKSDVWSF 426
 QY 411 GVLLMEFSGRAPPYPMMSLKEVSEAVENKGRMEPPGCGPVHVLSSCWEAEAPRRAP 470
 Db 427 GILTLFETVHGRIPPEMTNPEVIONLERGYRMVRPDCPEELIYQIMRLCKWKEPEDRPT 486
 QY 471 FRRLAERL 478
 Db 487 FDLRLSVL 494

RESULT 13

protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus
 C:Species: Rous sarcoma virus
 C>Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 04-Mar-2000
 C:Accession: S52313
 R:Yatouyan, A.; Yatoula, B.; Shultman, M.; Molinova, E.; Kaverina, I.; Musatkina, E.; Les
 submitted to the EMBL Data Library, January 1995
 A:Description: Two new isoforms of v-src oncogene isolated from low and high metastatic
 A:Reference number: S52313
 A:Accession: S52313
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-545 <TA1>
 A:Cross-references: EMBL:X84074; NID:g663083; PIDN:CA58881.1; PID:g663084
 C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h
 C:Keywords: ATP; autophosphorylation; blocked amino end; 11potein; myristylation; pnc
 F:108-157/Domain: SH3 homology <SH3>
 F:168-265/Domain: SH2 homology <SH2>
 F:285-543/Domain: protein kinase homology <KIN>
 F:293-301/Region: protein kinase ATP-binding motif
 F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F:315/Active site: Lys #status predicted
 F:436/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 27.6%; Score 736; DB 2; Length 545;
 Best Local Similarity 35.6%; Pred. No. 7.3e-31;

Matches 187; Conservative 82; Mismatches 181; Indels 76; Gaps 16;

QY 14 HGCDSAEELPR-----VSPRFLRANHP-----PYSARNPRTIRMACT----- 51
 Db 26 HGGFPASQTPNKAPLTAAPRSSR--RPPASQHRAPADTHRPSSRF--GYANBEKLE 81
 QY 52 -----QCLTKCEHTPPKPG-----ELAFRGADVTTILEACENKSWYR 88
 Db 82 GDFNTSDTYTSPGRATTLGAGVTTFVALDYDESMIETDLSFKGERQIYNNNEG--NWL 140
 QY 89 VKHHTSGQEGSLAAGALREKALSDAPKISLMPWFRKISGQAVOOLQPPED--GLFLV 146
 Db 141 AHSVTLTGQNGYIPSNVAPSDSIQAE-----EMWFGKILTRBSGRILLPENPRGFLV 194
 QY 147 RESARRHPGDVVLCS-----FGRDVIHYHVLHND--GLTIIDEAVFCNLMDEVHNSK 200

Db 195 RESETTKGAVACLSVDFDNAKGLNKHVYKIRKLDSCGFYTSRTQPSISQQLVAYYSKHA 254
 QY 201 GAICTLL--VPRRKIKGTSABEELARAGWLLNLQHLTGAQOGBEPGAVLQGEYLQ-Q 257
 Db 255 DGLCHRLTNVCPSPSKPOTOG---LAKDMEIPRESLRLEVKGQCCFEVWNGTWGTT 310
 QY 258 KVAYKNIK-CDVTAQAFIDEFAVMTKMOHENLVRLGLVTLHGLYIVMEHNSKGLVNF 316
 Db 311 RVAIKTLGQTHSPPEAFLOEAOVYMKLRHEKLVOLTAAYVSEBITYIVETMSGSLNFL 370
 QY 317 RTRGRALVNTAQLLOFSLHVAEGMEYLESKLVHNDLAARNILVSEDLVAVVSDFGAKA 376
 Db 371 KGEVGYTLRLPOLVDMAAQIASGMAYVERMNVYHRLRAANILVGENECKVADFGIARL 430
 QY 377 ----ERKGLDSSRLPVKWTAPDALKHGFTSKSDVWSFVLLMEVPSGRAPRKSLKE 432
 Db 431 IEDNEYTARQGAFAFPKWTAPDALKHGFTSKSDVWSFVLLMEVPSGRAPRKSLKE 490
 QY 433 VSEAVKGYRMEPPGCGPVHVLSSCWEAEAPRRAPPRKLAERL 478
 Db 491 VLDRVERGYRMPCPECPESLHDLMOQCMRREPEREPTREYLAQL 536

RESULT 14

TVCHS

protein-tyrosine kinase (EC 2.7.1.112) src - chicken
 N:Alternate names: kinase-related transforming protein src
 C:Species: Gallus gallus (chicken)
 C>Date: 19-Feb-1984 #sequence_revision 07-Oct-1994 #text_change 21-Jul-2000
 C:Accession: A00630; 150217; A41256; C35650; A32432
 R:Takeya, T.; Hanafusa, H.
 Cell 32, 881-890, 1983
 A:Title: Structure and sequence of the cellular gene homologous to the RSV sec gene a
 A:Reference number: A00630; M01D:83155664; PM1D:6295980
 A:Accession: A00630
 A:Molecule type: DNA
 A:Residues: 1-500, R, 502-533 <TA2>
 A:Cross-references: GB:J00844; NID:g212700
 R:Takeya, T.; Hanafusa, H.
 Cell 34, 319, 1983
 A:Reference number: A90838
 A:Contents: annotation; erratum, correct translation of residue 526
 R:Takeya, T.; Hanafusa, H.
 J. Virol. 44, 12-18, 1982
 A:Title: DNA sequence of the viral and cellular src gene of chickens: II comparison o
 A:Reference number: I50217; M01D:83059861; PM1D:6292480
 A:Accession: I50217
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-7 <TA2>
 A:Cross-references: GB:J00908; NID:g211690; PIDN:AAA48732.1; PID:g211691
 A:Note: the authors translated the codons AAC and CAG for residues 301 and 526 as Thr
 R:Doral, T.; Levy, J.B.; Kang, L.; Brugge, J.S.; Wang, L.H.
 Mol. Cell. Biol. 11, 4165-4176, 1991
 A:Title: Analysis of cDNAs of the proto-oncogene c-src: heterogeneity in 5' exons and
 A:Reference number: A41256; M01D:91304409; PM1D:1712905
 A:Accession: A41256
 A:Molecule type: mRNA
 A:Residues: 484-533 <DOR1>
 A:Cross-references: GB:S43579; NID:g1679964; PIDN:AAA19353.1; PID:g233061
 A:Note: the authors translated the codon CAG for residue 527 as Glu
 R:Doral, T.; Wang, L.H.
 Mol. Cell. Biol. 10, 4068-4079, 1990
 A:Title: An alternative non-tyrosine protein kinase product of the c-src gene in chlc
 A:Reference number: A35650; M01D:90318371; PM1D:2115117
 A:Accession: C35650
 A:Molecule type: mRNA
 A:Residues: 1-182, 'DPC1PLPSCLC' <DOR2>
 A:Cross-references: GB:M57290; NID:g212703; PIDN:AAA49078.1; PID:g212706
 A:Note: alternatively spliced mRNA exclusively replaces the long form in skeletal mus
 R:Shenoy, S.; Choi, J.K.; Bagrodia, S.; Copeland, T.D.; Maller, J.L.; Shalloway, D.

A:Cross-references: GB:I29119; GB:J02018; GB:J02026; GB:J02352; GB:K01194; GB:K01195;
R:Takeya, T.; Hanafusa, H.
Cell 32, 881-890, 1983
A>Title: Structure and sequence of the cellular gene homologous to the RSV sec gene a
Nucleic Acids Res. 17, 1252, 1989
A:Reference number: A00630; MUID:83155664; PMID:6299580
A:Accession: A00631
A:Molecule type: DNA
A:Residues: 1-62, 'D', '64-95, 'T', '97-123, 'V', '125-300, 'N', '302-526 <TA>
A:Experimental source: Strain Schmidt-Ruppin
R:Banier, J.V.; Dezeloe, P.; Marx, M.; Calochy, G.
A>Title: Nucleotide sequence of the src gene of the Schmidt-Ruppin strain of Rous Sarcoma Virus
Nucleic Acids Res. 17, 1252, 1989
A:Reference number: S02726; MUID:89160256; PMID:2537953
A:Accession: S02726
A:Molecule type: DNA
A:Residues: 1-9, 'G', '11-62, 'D', '64-123, 'V', '125-319, 'K', '321-495, 'S', '497-526 <BA>
A:Cross-references: EMBL:X13745; NID:g210187; PIDN:AAA42565.1; PID:g210189
R:Takeya, T.; Feldman, R.A.; Hanafusa, H.
J. Virol. 44, 1-11, 1982
A>Title: DNA sequence of the viral and cellular src gene of chickens. I. Complete nucleotide sequence of the viral src gene
Nucleic Acids Res. 10, 111-122, 1982
A:Reference number: A38018; MUID:83059858; PMID:6292477
A:Accession: A38018
A:Molecule type: DNA
A:Residues: 1-15, 'C', '17-94, 'RT', '97-116, 'D', '118-337, 'T', '339-526 <TA>
A:Cross-references: GB:K00928; NID:g210187; PIDN:AAA42565.1; PID:g210189
A:Experimental source: Strain RASV441
R:Nell, J.C.; Ghysdael, J.; Vogt, P.K.; Smart, J.E.
Nature 291, 675-677, 1981
A>Title: Homologous tyrosine phosphorylation sites in transformation-specific gene products of Rous sarcoma virus and avian myeloblastosis virus
Mol. Cell. Biol. 1, 111-119, 1981
A:Reference number: A38019; MUID:81220979; PMID:6264320
A:Contents: annotation: phosphorylation site
C:Comment: The sequence from the Schmidt-Ruppin strain is shown.
C:Genetics:
A:Gene: src
C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH2 domain; ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; F:148-245/Domain: SH3 homology <SH3>
F:148-245/Domain: SH2 homology <SH2>
F:265-523/Domain: protein kinase homology <KIN>
F:273-281/Region: protein kinase ATP-binding motif
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:295/Active site: Lys #status predicted
F:416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status expected

Query Match 27.5%; Score 734.5; DB 1; Length 526;
Best Local Similarity 39.2%; Pred. No. 8.4e-31;
Matches 168; Conservative 78; Mismatches 156; Indels 27; Gaps 10;

OY 66 ELAFRKGDVTILEACENKSMYRVKNHTSGOEGLLAGALEREALSADPKSLMPWFHG 125
 :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 99 DLSEKKGERILOIVNNTTEG-NMMVLHSLITGGOTGYIPSNVYAPSDIOAE-----EWYFG 151
 :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 126 KISQGEAVFOOLQRPED--GLFLVESANHPDDYLVCY-----GGRDVTHRYLVLRD-GH 177
 ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 152 KITRESRRLLNDENPRGTPLVRESEPTTKATCLISVSDFPNNAKGLNKHKKIKRLDSGC 211
 ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 178 LTIDEAVFFCNLMDMVENHSKDKAICTKL-VVRKRKHGTSAAEELARAGWLTLOHL 235
 ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 212 FYITSRNQSSLIQLDLVAAYSKHADGLCHRLTNVCPSTSPKQNG----LAKDAWEIPIRESL 267
 ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 236 TLGAQIGEGRGCAVLOGEFTLG-QKVAVYNKRC-DVTQAQELDEFRAVMYMKMGHNHNVTLG 293
 ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 268 RLEVKLVGGCGEGEWMWGWTGNCTTRVALKTTLPGTNSPFAELOAOVMKKLHHEKILVOLYA 327
 ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 294 VILHQGLTYIVAEHYSKGNLVNFLTREGRALVNTAQLLOFSLHVAEGMEYLESKLVNRDL 353
 ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 328 VVSEPELYIVIEYMSKSLDELFLGEMGKYLRLPDLVDMAQNLISGMAYVERBNMYVNRDL 387
 ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 354 AARNILVSEDILVAKVSDFLAKA---ERKGLDSSRLPYKKTATPADEALKHGKFTSKSDWS 409
 ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 388 RAANILVGENTVCKVADFGIALRLIEDNEYTRAOGCAKPKIKWTAFEAALYGRFTTIKSIDSWS 447

QY 410 FGVLLWEVFSYGRAPYPMKSLKEVSEAVEKGYRMEPEEGCGPYVHVLMSSCWEAEAPARR 469
||:| | : | | | | : | | | | : | | | | : | | | |
Db 448 FGILLPELTITKGRVPYPMGNGEVLDRVERGYRMPCEPCPESLHDLMOQWRRDPERRP 507
QY 470 PFRKLAERL 478
| | : |
Db 508 TFEYLOAOL 516

Search completed: July 29, 2003, 09:53:03
Job time : 25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2003, 09:51:02 ; Search time 27 Seconds
(without alignments)
2230.045 Million cell updates/sec

Title: US-09-977-261-2

Perfect score: 2671
Sequence: 1 MAGRGLSVNRAFHGCDSEAF.....PASVSGDADGSPRSQEP 507

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 118759770 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCR_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCRUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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- 16: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|------------------|--------------------|
| 1 | 2671 | 100.0 | 507 | US-09-977-269-2 | Sequence 2, Appl1 |
| 2 | 2671 | 100.0 | 507 | US-09-977-260-2 | Sequence 2, Appl1 |
| 3 | 2671 | 100.0 | 507 | US-09-977-261-2 | Sequence 2, Appl1 |
| 4 | 1245.5 | 46.6 | 450 | US-09-977-269-7 | Sequence 7, Appl1 |
| 5 | 1245.5 | 46.6 | 450 | US-09-977-260-7 | Sequence 7, Appl1 |
| 6 | 1245.5 | 46.6 | 450 | US-09-977-261-7 | Sequence 7, Appl1 |
| 7 | 1245.5 | 46.6 | 450 | US-10-059-585-42 | Sequence 42, Appl1 |
| 8 | 1245.5 | 46.6 | 450 | US-10-177-293-88 | Sequence 88, Appl1 |
| 9 | 1245.5 | 46.6 | 450 | US-10-298-377A-2 | Sequence 2, Appl1 |
| 10 | 916 | 34.3 | 357 | US-09-929-265-9 | Sequence 9, Appl1 |
| 11 | 768 | 28.8 | 258 | US-09-840-704-3 | Sequence 3, Appl1 |
| 12 | 742.5 | 27.8 | 509 | US-09-977-269-18 | Sequence 18, Appl1 |
| 13 | 742.5 | 27.8 | 509 | US-09-977-260-18 | Sequence 18, Appl1 |
| 14 | 742.5 | 27.8 | 509 | US-09-977-261-18 | Sequence 18, Appl1 |
| 15 | 727 | 27.2 | 536 | US-09-977-269-13 | Sequence 13, Appl1 |

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|----|-------|------|-----|----|--------------------|---------------------|
| 16 | 727 | 27.2 | 536 | 10 | US-09-977-260-13 | Sequence 13, Appl1 |
| 17 | 727 | 27.2 | 536 | 11 | US-09-929-266-10 | Sequence 10, Appl1 |
| 18 | 727 | 27.2 | 536 | 11 | US-09-977-261-13 | Sequence 13, Appl1 |
| 19 | 720.5 | 27.0 | 505 | 9 | US-09-977-269-17 | Sequence 17, Appl1 |
| 20 | 720.5 | 27.0 | 505 | 10 | US-09-977-260-17 | Sequence 17, Appl1 |
| 21 | 720.5 | 27.0 | 505 | 11 | US-09-977-261-17 | Sequence 17, Appl1 |
| 22 | 710 | 26.6 | 543 | 9 | US-09-977-269-14 | Sequence 14, Appl1 |
| 23 | 710 | 26.6 | 543 | 10 | US-09-977-260-14 | Sequence 14, Appl1 |
| 24 | 710 | 26.6 | 543 | 11 | US-09-977-261-14 | Sequence 14, Appl1 |
| 25 | 710 | 26.6 | 543 | 16 | US-10-298-377A-4 | Sequence 16, Appl1 |
| 26 | 707 | 26.5 | 512 | 9 | US-09-977-269-16 | Sequence 16, Appl1 |
| 27 | 707 | 26.5 | 512 | 10 | US-09-977-260-16 | Sequence 16, Appl1 |
| 28 | 707 | 26.5 | 512 | 11 | US-09-977-261-16 | Sequence 16, Appl1 |
| 29 | 699.5 | 26.2 | 536 | 9 | US-09-977-269-12 | Sequence 12, Appl1 |
| 30 | 699.5 | 26.2 | 536 | 10 | US-09-977-260-12 | Sequence 12, Appl1 |
| 31 | 699.5 | 26.2 | 536 | 11 | US-09-977-261-12 | Sequence 12, Appl1 |
| 32 | 699 | 26.2 | 499 | 9 | US-09-977-269-19 | Sequence 19, Appl1 |
| 33 | 699 | 26.2 | 499 | 10 | US-09-977-260-19 | Sequence 19, Appl1 |
| 34 | 699 | 26.2 | 499 | 11 | US-09-977-261-19 | Sequence 19, Appl1 |
| 35 | 698.5 | 26.2 | 537 | 9 | US-09-977-269-11 | Sequence 11, Appl1 |
| 36 | 698.5 | 26.2 | 537 | 10 | US-09-977-260-11 | Sequence 11, Appl1 |
| 37 | 698.5 | 26.2 | 537 | 11 | US-09-977-261-11 | Sequence 11, Appl1 |
| 38 | 695.5 | 26.0 | 537 | 10 | US-09-771-161A-212 | Sequence 212, Appl1 |
| 39 | 695.5 | 26.0 | 537 | 10 | US-09-771-161A-213 | Sequence 213, Appl1 |
| 40 | 692 | 25.9 | 505 | 10 | US-09-771-161A-186 | Sequence 186, Appl1 |
| 41 | 681.5 | 25.5 | 529 | 9 | US-09-977-269-15 | Sequence 15, Appl1 |
| 42 | 681.5 | 25.5 | 529 | 10 | US-09-977-260-15 | Sequence 15, Appl1 |
| 43 | 681.5 | 25.5 | 529 | 11 | US-09-977-261-15 | Sequence 15, Appl1 |
| 44 | 660.5 | 24.7 | 822 | 14 | US-10-003-295-4 | Sequence 4, Appl1 |
| 45 | 654.5 | 24.5 | 505 | 9 | US-09-977-269-6 | Sequence 6, Appl1 |

ALIGNMENTS

| | | | | | | | | | |
|---|-----|---|-----|--|--|--|--|--|--|
| RESULT 1 | | | | | | | | | |
| US-09-977-269-2 | | | | | | | | | |
| Sequence 2, Application US/09977269 | | | | | | | | | |
| Patent No. US20020082037A1 | | | | | | | | | |
| GENERAL INFORMATION: | | | | | | | | | |
| APPLICANT: ULIRICH, AXEL | | | | | | | | | |
| APPLICANT: GISHIZKY, MIKHAIL | | | | | | | | | |
| APPLICANT: SUDES, IRINGARD | | | | | | | | | |
| TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES | | | | | | | | | |
| FILE REFERENCE: 038602/1260 | | | | | | | | | |
| CURRENT APPLICATION NUMBER: US/09/977, 269 | | | | | | | | | |
| CURRENT FILING DATE: 2001-10-16 | | | | | | | | | |
| PRIOR APPLICATION NUMBER: 08/232,545 | | | | | | | | | |
| PRIOR FILING DATE: 1994-04-22 | | | | | | | | | |
| NUMBER OF SEQ ID NOS: 24 | | | | | | | | | |
| SOFTWARE: PatentIn Ver. 2.1 | | | | | | | | | |
| SEQ ID NO 2 | | | | | | | | | |
| LENGTH: 507 | | | | | | | | | |
| TYPE: PRT | | | | | | | | | |
| ORGANISM: Unknown Organism | | | | | | | | | |
| FEATURE: Unknown Organism | | | | | | | | | |
| OTHER INFORMATION: Description of Unknown Organism: Megakaryocyte | | | | | | | | | |
| OTHER INFORMATION: Kinase 1 | | | | | | | | | |
| US-09-977-269-2 | | | | | | | | | |
| Query Match | | | | | | | | | |
| Best Local Similarity 100.0%; Score 2671; DB 9; Length 507; | | | | | | | | | |
| Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | | | | | | | |
| Qy | 1 | MAGRGLSVNRAFHGCDSEAFPRVSPRFLRAMHPVVSAMPTRRNAPGTCITKCEHT | 60 | | | | | | |
| Qy | 1 | MAGRGLSVNRAFHGCDSEAFPRVSPRFLRAMHPVVSAMPTRRNAPGTCITKCEHT | 60 | | | | | | |
| Db | 1 | MAGRGLSVNRAFHGCDSEAFPRVSPRFLRAMHPVVSAMPTRRNAPGTCITKCEHT | 60 | | | | | | |
| Qy | 61 | RPRFGELAFRRGDVVTLLACENKSWYRVKHHTSGGGLLAAGLRERALSADPKSLM | 120 | | | | | | |
| Qy | 61 | RPRFGELAFRRGDVVTLLACENKSWYRVKHHTSGGGLLAAGLRERALSADPKSLM | 120 | | | | | | |
| Db | 61 | RPRFGELAFRRGDVVTLLACENKSWYRVKHHTSGGGLLAAGLRERALSADPKSLM | 120 | | | | | | |
| Qy | 121 | PMFNGKLSGGEAIVQQLPREDGLFLVRESARHPEDVILCVSFGNDVYHYRLHMDGLITI | 180 | | | | | | |

```

Db      121 PMFHGKISGOEAVOOLPPEDGLFVRESARHPGDVLCVSGRDVTHRVLRHDSGLTI 180
Qy      181 DEAVFFCNLMADWNEHYSKDKGALCTKLVPRKRKHGTFKSABEELARAGWMLNLOHLTLGAQ 240
Db      181 DEAVFFCNLMADWNEHYSKDKGALCTKLVPRKRKHGTFKSABEELARAGWMLNLOHLTLGAQ 240
Qy      241 IGEFEGGAVLQGEYLGOKVAVNKIKCDVTAQAFLEDTAVMTKMQHENVLLGLVLIHQGL 300
Db      241 IGEFEGGAVLQGEYLGOKVAVNKIKCDVTAQAFLEDTAVMTKMQHENVLLGLVLIHQGL 300
Qy      301 YIWEHVSCKGNLVNFTLRGRALVNTAQLLOFSLHVAEGMEYLESKKLVHRDLAARNILV 360
Db      301 YIWEHVSCKGNLVNFTLRGRALVNTAQLLOFSLHVAEGMEYLESKKLVHRDLAARNILV 360
Qy      361 SEDLVAKVSDPGLAKAEKRGDSSRLPVKWTAPALKHGFTSKSDVMSFGVLLMEVFSY 420
Db      361 SEDLVAKVSDPGLAKAEKRGDSSRLPVKWTAPALKHGFTSKSDVMSFGVLLMEVFSY 420
Qy      421 GRAPYPMKSLKEVSEAVEKGYRMEPEGCPCGPVHVLMSCWEAEAPARRPFRKLAEKLAR 480
Db      421 GRAPYPMKSLKEVSEAVEKGYRMEPEGCPCGPVHVLMSCWEAEAPARRPFRKLAEKLAR 480
Qy      481 ELRSAGAPASVSGODADGSTSPRSQEP 507
Db      481 ELRSAGAPASVSGODADGSTSPRSQEP 507

```

RESULT 2

```

US-09-977-260-2
; Sequence 2, Application US/09977260
; Publication No. US20020192790A1
; GENERAL INFORMATION:
; APPLICANT: ULLRICH, AXEL
; APPLICANT: GISHIZKY, MIKHAIL
; APPLICANT: SURES, IRMINGARD
; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
; FILE REFERENCE: 038602/1260
; CURRENT APPLICATION NUMBER: US/09/977, 260
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 08/232, 545
; PRIOR FILING DATE: 1994-04-22
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Megakaryocyte
; OTHER INFORMATION: kinase 1
US-09-977-260-2

```

```

Query Match      100.0%; Score 2671; DB 10; Length 507;
Best Local Similarity 100.0%; Pred. No. 6, 7e-209;
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 MAGRGSLSVSWRAFHGCDSEAEELPRVSPRFLRAWHPPVSAARMPTRRMAPGTQCTITKCEHT 60
Db      1 MAGRGSLSVSWRAFHGCDSEAEELPRVSPRFLRAWHPPVSAARMPTRRMAPGTQCTITKCEHT 60
Qy      61 RRPFGELARPKGDVVTITLACENKSWRYKHNHTSGOGLIAGALRERALSADPKLSLM 120
Db      61 RRPFGELARPKGDVVTITLACENKSWRYKHNHTSGOGLIAGALRERALSADPKLSLM 120
Qy      121 PMFHGKISGOEAVOOLPPEDGLFVRESARHPGDVLCVSGRDVTHRVLRHDSGLTI 180
Db      121 PMFHGKISGOEAVOOLPPEDGLFVRESARHPGDVLCVSGRDVTHRVLRHDSGLTI 180
Qy      181 DEAVFFCNLMADWNEHYSKDKGALCTKLVPRKRKHGTFKSABEELARAGWMLNLOHLTLGAQ 240
Db      181 DEAVFFCNLMADWNEHYSKDKGALCTKLVPRKRKHGTFKSABEELARAGWMLNLOHLTLGAQ 240

```

```

Qy      241 IGEFEGGAVLQGEYLGOKVAVNKIKCDVTAQAFLEDTAVMTKMQHENVLLGLVLIHQGL 300
Db      241 IGEFEGGAVLQGEYLGOKVAVNKIKCDVTAQAFLEDTAVMTKMQHENVLLGLVLIHQGL 300
Qy      301 YIWEHVSCKGNLVNFTLRGRALVNTAQLLOFSLHVAEGMEYLESKKLVHRDLAARNILV 360
Db      301 YIWEHVSCKGNLVNFTLRGRALVNTAQLLOFSLHVAEGMEYLESKKLVHRDLAARNILV 360
Qy      361 SEDLVAKVSDPGLAKAEKRGDSSRLPVKWTAPALKHGFTSKSDVMSFGVLLMEVFSY 420
Db      361 SEDLVAKVSDPGLAKAEKRGDSSRLPVKWTAPALKHGFTSKSDVMSFGVLLMEVFSY 420
Qy      421 GRAPYPMKSLKEVSEAVEKGYRMEPEGCPCGPVHVLMSCWEAEAPARRPFRKLAEKLAR 480
Db      421 GRAPYPMKSLKEVSEAVEKGYRMEPEGCPCGPVHVLMSCWEAEAPARRPFRKLAEKLAR 480
Qy      481 ELRSAGAPASVSGODADGSTSPRSQEP 507
Db      481 ELRSAGAPASVSGODADGSTSPRSQEP 507

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RESULT 3

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US-09-977-261-2
; Sequence 2, Application US/09977261
; Publication No. US20030054527A1
; GENERAL INFORMATION:
; APPLICANT: ULLRICH, AXEL
; APPLICANT: GISHIZKY, MIKHAIL
; APPLICANT: SURES, IRMINGARD
; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
; FILE REFERENCE: 038602/1259
; CURRENT APPLICATION NUMBER: US/09/977, 261
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 08/232, 545
; PRIOR FILING DATE: 1994-04-22
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Megakaryocyte
; OTHER INFORMATION: kinase 1
US-09-977-261-2

```

```

Query Match      100.0%; Score 2671; DB 11; Length 507;
Best Local Similarity 100.0%; Pred. No. 6, 7e-209;
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MAGRGSLSVSWRAFHGCDSEAEELPRVSPRFLRAWHPPVSAARMPTRRMAPGTQCTITKCEHT 60
Db      1 MAGRGSLSVSWRAFHGCDSEAEELPRVSPRFLRAWHPPVSAARMPTRRMAPGTQCTITKCEHT 60
Qy      61 RRPFGELARPKGDVVTITLACENKSWRYKHNHTSGOGLIAGALRERALSADPKLSLM 120
Db      61 RRPFGELARPKGDVVTITLACENKSWRYKHNHTSGOGLIAGALRERALSADPKLSLM 120
Qy      121 PMFHGKISGOEAVOOLPPEDGLFVRESARHPGDVLCVSGRDVTHRVLRHDSGLTI 180
Db      121 PMFHGKISGOEAVOOLPPEDGLFVRESARHPGDVLCVSGRDVTHRVLRHDSGLTI 180
Qy      181 DEAVFFCNLMADWNEHYSKDKGALCTKLVPRKRKHGTFKSABEELARAGWMLNLOHLTLGAQ 240
Db      181 DEAVFFCNLMADWNEHYSKDKGALCTKLVPRKRKHGTFKSABEELARAGWMLNLOHLTLGAQ 240
Qy      241 IGEFEGGAVLQGEYLGOKVAVNKIKCDVTAQAFLEDTAVMTKMQHENVLLGLVLIHQGL 300
Db      241 IGEFEGGAVLQGEYLGOKVAVNKIKCDVTAQAFLEDTAVMTKMQHENVLLGLVLIHQGL 300
Qy      301 YIWEHVSCKGNLVNFTLRGRALVNTAQLLOFSLHVAEGMEYLESKKLVHRDLAARNILV 360
Db      301 YIWEHVSCKGNLVNFTLRGRALVNTAQLLOFSLHVAEGMEYLESKKLVHRDLAARNILV 360

```

```

US-09-977-260-7
? Sequence 7, Application US/09977260
? Publication No. US20020192790A1
? GENERAL INFORMATION:
? APPLICANT: ULRICH, AXEL
? APPLICANT: GISHITZY, MIKHAIL
? APPLICANT: SURES, IRMINGARD
? TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
? FILE REFERENCE: 038602/1260
? CURRENT APPLICATION NUMBER: US/09/977, 260
? CURRENT FILING DATE: 2001-10-16
? PRIOR APPLICATION NUMBER: 08/232,545
? PRIOR FILING DATE: 1994-04-22
? NUMBER OF SEQ ID NOS: 24
? SOFTWARE: Patentin Ver. 2.1
? SEQ ID NO 7
? LENGTH: 450
? TYPE: PRT
? ORGANISM: Homo sapiens
US-09-977-260-7

Query Match          46.6%; Score 1245.5; DB 10; Length 450;
Best Local Similarity 54.1%; Pred. No. 4.4e-93;
Matches 235; Conservative 81; Mismatches 115; Indels 3; Gaps 2

QY 47 WAPSTOCITKCEHTRPRKPELAFRKGDVVTLLEACENKSRVVKHHTSGOEGILAAAGLR 106
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 8 WPSGTCEKAKTNFNGTAAQDLPFCCKGDVLTITVAVKDPNWKAKKKV-GREGIIPANYQ 66
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 107 EREALSADPKLSTMPWFHGKTSQGEAVVOOQDPEDGELVYRESARHPGQDYLCVSFGRDY 166
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 67 KREGVKAQTKLSTMPWFHGKITYREQAERLLYPPETGLFLVRESTDYPPDDYTLVCSCDGKV 126
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 167 IHYRLHGDHULTIDEAVFPCNLDMVMEHYSKDKAICTKTVLRPRKRGTKSAEEELARA 226
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 127 EHYRIMYASKLSTIDEVYFENLMQVYHRTSDADGICTRLIKPRVMECTYVAADPEFRS 186
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 227 GWMLNLQHLTLGAOIGEGSEFGAVLOGEYLQGRVAVAKNIKCDVTAQAFLEDETAVMTKMOHE 286
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 187 GWALNMKELKLTQITGKGEFGDVMIGDYRGKKVAVKCIKNDATAQAFLEASVMTOLRRS 246
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 287 NLVRLGLYILMQ--GLTYKMEHVSNGNLVNLRTGRGALVNTAQLQSSLAHAEEMYLE 344
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 247 NLVOLLGTYVEKGGLYTYTEYMAKGSJVDYLRSGRSVLGGDCLKFSLDVCEAMEYLE 306
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 345 SKKLVRDLARNLIVSEDLVAAKVSDFGLAAERKGLDSSRLPYKMTAPEALKHGKFTSK 404
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 307 GNNFVHRDLARNLIVSEDLVAAKVSDFGLTYEASTDPTGKLPVMTAPEALREKKFSTK 366
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 405 SDVASFVGLMEVSYGRAPYPKMSLKLSVSEAVEKGYEMEPPEGCGPVHVLMSSCWEAE 464
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 367 SDVASFGLMEVSYGRAPYPRIPRLKQVYVREVEKGYMDADPGCPRAVYEVKMKCWMLD 426
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 465 PARPPEPKLAELK 478
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 427 AAMRPSFLQLEOL 440
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 6
US-09-977-261-7
? Sequence 7, Application US/09977261
? Publication No. US20030054527A1
? GENERAL INFORMATION:
? APPLICANT: ULRICH, AXEL
? APPLICANT: GISHITZY, MIKHAIL
? APPLICANT: SURES, IRMINGARD
? TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
? FILE REFERENCE: 038602/1259
? CURRENT APPLICATION NUMBER: US/09/977, 261
? CURRENT FILING DATE: 2001-10-16
? PRIOR APPLICATION NUMBER: 08/232,545
? PRIOR FILING DATE: 1994-04-22

```

NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
LENGTH: 450
TYPE: PRT
ORGANISM: Homo sapiens
US-09-977-261-7

Query Match 46.6%; Score 1245.5; DB 11; Length 450;
Best Local Similarity 54.1%; Pred. No. 4.4e-93;
Matches 235; Conservative 81; Mismatches 115; Indels 3; Gaps 2;

47 WAPGTCTCCEHTRPKPELAFRKGDVVTILEACENKSMYRVKHNHTSGOGLAAGALR 106
1 WPGSTCTCIKYNFHGTAEDLPFCCKGDVLTIVAVTKDPMYKAKNKV-GREGIIPANYQ 66
107 EREALSADPKLSLMPFHGKISGQEAVALQDPEDGLFVRESARHPGDVILCVSFGRDY 166
67 KREGVAGTKLSLMPFHGKITREQAERLLYPETGLFVRESTNPGDYTLGVSCDGRV 126
167 IHYRVLRHGHLLTIDAVFECNLMQVENVHNSKDKGAICTKLVPKRKHGTSAAEELARA 226
127 EHRIRYHASKSLIDEVEFENLMQVENVHNSKDKGAICTKLVPKRKHGTSAAEELARA 186
227 GWLNLQHLTLGAQIEGEGFAGVLOGEYLGQKVAANKICDVTAAQAFDELTAVMTKQHE 286
187 GWALNKKELKLTQITKGEFGDVMGIDYGNKVAVCIKNDATAQAFLEASVMTQLRHS 246
287 NIVRLIGVTLHQ--GLIYMEHVSCKNLVNLTRGRALVNTAQLQSLHVAEGMEYLE 344
247 NIVQLLGAVIIEEGGLIYTEYMAKSLVDYLRSGRSVYAGDCLTKFSLDCEAMEYLE 306
345 SKKLVRDLAARNILVSEDLVAKVSDFGLAKEKRGKJDSRLPVKWTAPALKHGFTSK 404
307 GNNFVHRDLAARNVLSSEDAVAKVSDFGLTKEASTQDTGKLPVKTAPALREKKEFTSK 366
405 SDVMSFGVLLMEYFSYGRAPYKMSLKEVSEAVEKGRMEPPGCGPVAHVLSSCWEAE 464
367 SDVMSFGVLLMEYFSYGRAPYKMSLKEVSEAVEKGRMEPPGCGPVAHVLSSCWEAE 426
465 PARPPFRKLAETL 478
427 AAMRPSFLQRL 440

RESULT 7
US-10-059-585-42
Sequence 42. Application US/10059585
Publication No. US20030082776A1
GENERAL INFORMATION:
APPLICANT: Ota, Toshio
APPLICANT: Isogai, Takao
APPLICANT: Nishikawa, Tetsuo
APPLICANT: Hayashi, Koji
APPLICANT: Otsuka, Kaoru
APPLICANT: Yamamoto, Jun-ichi
APPLICANT: Ishii, Shizuko
APPLICANT: Sugiyama, Tomoyasu
APPLICANT: Wakamatsu, Ai
APPLICANT: Nagai, Keiichi
APPLICANT: Otsuki, Tetsuji
APPLICANT: Funahashi, Shin-ichi
APPLICANT: Senoo, Chiaki
APPLICANT: Nezu, Jun-ichi
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
TITLE OF INVENTION: KINASE/PROTEIN PHOSPHATASE
FILE REFERENCE: 06501-098001
CURRENT APPLICATION NUMBER: US/10/059,585
CURRENT FILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: PCT/JP00/05060
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/183,322
PRIOR FILING DATE: 2000-02-17

PRIOR APPLICATION NUMBER: US 60/159,590
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: JP 2000-118776
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: JP 2000-183767
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: JP 11-248036
PRIOR FILING DATE: 1999-07-29
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 42
LENGTH: 450
TYPE: PRT
ORGANISM: Homo sapiens
US-10-059-585-42

Query Match 46.6%; Score 1245.5; DB 15; Length 450;
Best Local Similarity 54.1%; Pred. No. 4.4e-93;
Matches 235; Conservative 81; Mismatches 115; Indels 3; Gaps 2;

47 WAPGTCTCCEHTRPKPELAFRKGDVVTILEACENKSMYRVKHNHTSGOGLAAGALR 106
8 WPGSTCTCIKYNFHGTAEDLPFCCKGDVLTIVAVTKDPMYKAKNKV-GREGIIPANYQ 66
107 EREALSADPKLSLMPFHGKISGQEAVALQDPEDGLFVRESARHPGDVILCVSFGRDY 166
67 KREGVAGTKLSLMPFHGKITREQAERLLYPETGLFVRESTNPGDYTLGVSCDGRV 126
167 IHYRVLRHGHLLTIDAVFECNLMQVENVHNSKDKGAICTKLVPKRKHGTSAAEELARA 226
127 EHRIRYHASKSLIDEVEFENLMQVENVHNSKDKGAICTKLVPKRKHGTSAAEELARA 186
227 GWLNLQHLTLGAQIEGEGFAGVLOGEYLGQKVAANKICDVTAAQAFDELTAVMTKQHE 286
187 GWALNKKELKLTQITKGEFGDVMGIDYGNKVAVCIKNDATAQAFLEASVMTQLRHS 246
287 NIVRLIGVTLHQ--GLIYMEHVSCKNLVNLTRGRALVNTAQLQSLHVAEGMEYLE 344
247 NIVQLLGAVIIEEGGLIYTEYMAKSLVDYLRSGRSVYAGDCLTKFSLDCEAMEYLE 306
345 SKKLVRDLAARNILVSEDLVAKVSDFGLAKEKRGKJDSRLPVKWTAPALKHGFTSK 404
307 GNNFVHRDLAARNVLSSEDAVAKVSDFGLTKEASTQDTGKLPVKTAPALREKKEFTSK 366
405 SDVMSFGVLLMEYFSYGRAPYKMSLKEVSEAVEKGRMEPPGCGPVAHVLSSCWEAE 464
367 SDVMSFGVLLMEYFSYGRAPYKMSLKEVSEAVEKGRMEPPGCGPVAHVLSSCWEAE 426
465 PARPPFRKLAETL 478
427 AAMRPSFLQRL 440

RESULT 8
US-10-177-293-88
Sequence 88. Application US/10177293
Publication No. US20030124128A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Glatz, Karen
APPLICANT: Zhao, Xumei
APPLICANT: Gannavarpu, Manjula
APPLICANT: Kamatkar, Shubhang
APPLICANT: Mertens, Maureen
APPLICANT: Meyer, Vic
APPLICANT: Wang, Youzhen
APPLICANT: Xu, Yongyao
APPLICANT: Hoersch, Sebastian
APPLICANT: Monahan, John
APPLICANT: Meyers, Rachel E.
APPLICANT: Bast Jr., Robert C.
APPLICANT: Hortobagyi, Gabriel N.
APPLICANT: Fustzai, Lajos

```
; APPLICANT: Meric, Funda
; APPLICANT: Sahin, Aysegul
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; FILE REFERENCE: PREVENTION, AND THERAPY OF BREAST CANCER
; CURRENT APPLICATION NUMBER: US/10/177,293
; PRIOR APPLICATION NUMBER: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-293-88
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Query Match 46.6%; Score 1245.5; DB 15; Length 450;
Best Local Similarity 54.1%; Pred. No. 4.4e-93;
Matches 235; Conservative 81; Mismatches 115; Indels 3; Gaps 2;
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```
QY 47 MARGTCITKCEHTRPRKPGELAFKRGDVTITLACEKMSYRVNHTSGOGLIAGALR 106
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
8 WPGSTECIAKYNFHGTAEDLPFCBGDVTITVATKDPNMYKAKNKV-GREGIIPANYQ 66
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 107 EREALSADPKLSLMPFHHGKISGOEAVOQLOPPEDGLFLYRESARHPGDVILCVSFGRDV 166
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
67 KREGVAGKGTSLMPFHHGKITRQEARLLYPETGTLVRESNINYPGDVTLVSCDGVY 126
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 167 IHYVLRDGHLLTIDEAVFCNLMDEVENHYSKDKGICTKLVPRKRKHGKRSABEELARA 226
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
127 EHYRIMYHASKLSIDEEVYFENIMQVLEHTSDADGICTRLIKPKVMEGTVAADDERYS 186
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 227 GWLNLQHLTLGAOIGEGEAVLOGEYLGOKYAVNKNIKCDVTAQAFLDETAVENTKQHE 286
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
187 GWALNMKELKLTQIGKEGEGDVMGDRGNKVAVKICKNDATAQAFLEASVMTOLRHS 246
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 287 NLVRLGLVILHQ--GLYIVMEHVSCKNLVFLTRGRALVNTAQLLOFSLHVAEGMYLE 344
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
247 NLVOLLGVIVEEKGLIYVEYMAKSLVDYLSRGRSVLGDCCLLFSLDVCBAMEYLE 306
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 345 SKKLVRHDLAARNILVSEDLVAVKSDFGGLAKAEKKGIDSSRLPYKWTAPALRKHGKETS 404
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
307 GNNFVHRDLAARNVLSSEDNVAKVSDGLTKKASSTODTGKLPVKWTAPALRKHGKETS 366
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 405 SDVMSFGVILMEVYSGRAPYPMKSLKEVSEAVEKGRMPPECCPGPVAVLMSCEAE 464
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
367 SDVMSFGVILMEVYSGRAPYPMKSLKEVSEAVEKGRMPPECCPGPVAVLMSCEAE 426
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 465 PARPPPRKLAELK 478
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 427 AAMRPSFLQRL 440
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
```

```
RESULT 9
US-10-298-377A-2
; Sequence 2, Application US/10298377A
; Publication No. US20030130209A1
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; APPLICANT: Chetesh, David A.
; APPLICANT: Paul, Robert
```

```
; APPLICANT: Elliceiri, Brian
; TITLE OF INVENTION: Method of Treatment of Myocardial
; FILE REFERENCE: Infarction
; CURRENT APPLICATION NUMBER: US/10/298,377A
; PRIOR APPLICATION NUMBER: 2002-11-18
; PRIOR APPLICATION NUMBER: 10/298,377
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/470,881
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: 09/538,248
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: PCT/US99/11780
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,220
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 450
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-298-377A-2
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Query Match 46.6%; Score 1245.5; DB 16; Length 450;
Best Local Similarity 54.1%; Pred. No. 4.4e-93;
Matches 235; Conservative 81; Mismatches 115; Indels 3; Gaps 2;
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QY 47 MARGTCITKCEHTRPRKPGELAFKRGDVTITLACEKMSYRVNHTSGOGLIAGALR 106
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
8 WPGSTECIAKYNFHGTAEDLPFCBGDVTITVATKDPNMYKAKNKV-GREGIIPANYQ 66
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 107 EREALSADPKLSLMPFHHGKISGOEAVOQLOPPEDGLFLYRESARHPGDVILCVSFGRDV 166
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
67 KREGVAGKGTSLMPFHHGKITRQEARLLYPETGTLVRESNINYPGDVTLVSCDGVY 126
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 167 IHYVLRDGHLLTIDEAVFCNLMDEVENHYSKDKGICTKLVPRKRKHGKRSABEELARA 226
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
127 EHYRIMYHASKLSIDEEVYFENIMQVLEHTSDADGICTRLIKPKVMEGTVAADDERYS 186
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 227 GWLNLQHLTLGAOIGEGEAVLOGEYLGOKYAVNKNIKCDVTAQAFLDETAVENTKQHE 286
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
187 GWALNMKELKLTQIGKEGEGDVMGDRGNKVAVKICKNDATAQAFLEASVMTOLRHS 246
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 287 NLVRLGLVILHQ--GLYIVMEHVSCKNLVFLTRGRALVNTAQLLOFSLHVAEGMYLE 344
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
247 NLVOLLGVIVEEKGLIYVEYMAKSLVDYLSRGRSVLGDCCLLFSLDVCBAMEYLE 306
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 345 SKKLVRHDLAARNILVSEDLVAVKSDFGGLAKAEKKGIDSSRLPYKWTAPALRKHGKETS 404
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
307 GNNFVHRDLAARNVLSSEDNVAKVSDGLTKKASSTODTGKLPVKWTAPALRKHGKETS 366
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 405 SDVMSFGVILMEVYSGRAPYPMKSLKEVSEAVEKGRMPPECCPGPVAVLMSCEAE 464
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
367 SDVMSFGVILMEVYSGRAPYPMKSLKEVSEAVEKGRMPPECCPGPVAVLMSCEAE 426
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 465 PARPPPRKLAELK 478
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 427 AAMRPSFLQRL 440
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
```

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RESULT 10
US-09-929-266-9
; Sequence 9, Application US/09929266
; Publication No. US20030045694A1
; GENERAL INFORMATION:
; APPLICANT: Brian T. Chait
; APPLICANT: Darin R. Latimer
; APPLICANT: Paul M. Lizardi
; APPLICANT: Eric R. Kershnar
; APPLICANT: Jon S. Morrow
; APPLICANT: Matthew E. Roth
; APPLICANT: Martin J. Mattessich
```


| | | | | |
|-------------|--------|------------|--------|-------------|
| Query Match | 28.8%; | Score 768; | DB 10; | Length 258; |
|-------------|--------|------------|--------|-------------|

DB 367 AANILVSDTLSCCKIADFGIARLLIEDNEXYAREGAKFPKWTAPPAINYGFTTIKSDVMSF 426


```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-977-269-13

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| | | | | |
|---------------------------|-------|-------------------|-----------|------------|
| Query Match | 27.28 | Score 727 | DB 9 | Length 536 |
| Best Local Similarity | 35.28 | Pred. No. 7.8e-51 | | |
| Matches 182, Conservative | 83 | Mismatches 178 | Indels 74 | Gaps 14 |

[illegible]

Search completed: July 29, 2003, 09:53:36
Job time : 29 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 29, 2003, 09:49:12 ; Search time 20 Seconds
(without alignments)
1072.580 Million cell updates/sec

Title: US-09-977-261-2
Perfect score: 2671
Sequence: 1 MAGRGLYSMAFHGCSAE.....PASVSGDADGSPRSQEP 507

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents-AA:*
1: /cgn2.6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2.6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2.6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2.6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2.6/ptodata/1/1aa/PCITUS.COMB.pep:*
6: /cgn2.6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|-------------------|--------------------|
| 1 | 2671 | 100.0 | 507 | US-08-426-509A-2 | Sequence 2, Appl1 |
| 2 | 2671 | 100.0 | 507 | US-08-232-545-2 | Sequence 2, Appl1 |
| 3 | 2671 | 100.0 | 507 | PCR-US95-05008-2 | Sequence 2, Appl1 |
| 4 | 2664 | 99.7 | 507 | US-08-604-989A-5 | Sequence 5, Appl1 |
| 5 | 2445 | 91.5 | 527 | US-09-315-928-2 | Sequence 2, Appl1 |
| 6 | 2444 | 91.5 | 466 | US-08-604-989A-4 | Sequence 2, Appl1 |
| 7 | 2434 | 91.1 | 466 | US-08-876-882-2 | Sequence 2, Appl1 |
| 8 | 2012 | 75.3 | 386 | US-09-741-154-4 | Sequence 4, Appl1 |
| 9 | 2012 | 75.3 | 415 | US-09-741-154-2 | Sequence 2, Appl1 |
| 10 | 1269 | 47.5 | 246 | US-08-604-989A-3 | Sequence 3, Appl1 |
| 11 | 1245.5 | 46.6 | 450 | US-08-426-509A-7 | Sequence 7, Appl1 |
| 12 | 1245.5 | 46.6 | 450 | US-08-232-545-7 | Sequence 7, Appl1 |
| 13 | 1245.5 | 46.6 | 450 | PCR-US95-05008-7 | Sequence 7, Appl1 |
| 14 | 797 | 29.8 | 269 | US-08-701-191A-35 | Sequence 35, Appl1 |
| 15 | 768 | 28.8 | 258 | US-09-035-706-3 | Sequence 3, Appl1 |
| 16 | 768 | 28.8 | 258 | US-08-955-841-3 | Sequence 3, Appl1 |
| 17 | 768 | 28.8 | 258 | US-09-390-425-3 | Sequence 3, Appl1 |
| 18 | 768 | 28.8 | 258 | US-09-566-906-3 | Sequence 3, Appl1 |
| 19 | 742.5 | 27.8 | 509 | US-09-039-555B-17 | Sequence 17, Appl1 |
| 20 | 742.5 | 27.8 | 509 | US-08-426-509A-18 | Sequence 18, Appl1 |
| 21 | 742.5 | 27.8 | 509 | US-09-457-040B-8 | Sequence 8, Appl1 |
| 22 | 742.5 | 27.8 | 509 | US-08-232-545-18 | Sequence 18, Appl1 |
| 23 | 742.5 | 27.8 | 509 | PCR-US95-05008-18 | Sequence 18, Appl1 |
| 24 | 732 | 27.4 | 533 | US-07-820-011A-2 | Sequence 2, Appl1 |
| 25 | 732 | 27.4 | 533 | PCR-US93-00445-2 | Sequence 2, Appl1 |
| 26 | 727 | 27.2 | 536 | US-07-820-011A-4 | Sequence 4, Appl1 |
| 27 | 727 | 27.2 | 536 | US-08-426-509A-13 | Sequence 13, Appl1 |

| | | | | | |
|----|-------|------|-----|-------------------|--------------------|
| 28 | 727 | 27.2 | 536 | US-08-232-545-13 | Sequence 13, Appl1 |
| 29 | 727 | 27.2 | 536 | PCR-US93-00445-4 | Sequence 4, Appl1 |
| 30 | 727 | 27.2 | 536 | PCR-US95-05008-13 | Sequence 13, Appl1 |
| 31 | 720.5 | 27.0 | 505 | US-08-426-509A-17 | Sequence 17, Appl1 |
| 32 | 720.5 | 27.0 | 505 | US-08-232-545-17 | Sequence 17, Appl1 |
| 33 | 720.5 | 27.0 | 505 | PCR-US95-05008-17 | Sequence 17, Appl1 |
| 34 | 710 | 26.6 | 543 | US-08-426-509A-14 | Sequence 14, Appl1 |
| 35 | 710 | 26.6 | 543 | US-08-232-545-14 | Sequence 14, Appl1 |
| 36 | 710 | 26.6 | 543 | PCR-US95-05008-14 | Sequence 14, Appl1 |
| 37 | 707 | 26.5 | 512 | US-08-426-509A-16 | Sequence 16, Appl1 |
| 38 | 707 | 26.5 | 512 | US-08-232-545-16 | Sequence 16, Appl1 |
| 39 | 707 | 26.5 | 512 | PCR-US95-05008-16 | Sequence 16, Appl1 |
| 40 | 699.5 | 26.2 | 536 | US-08-426-509A-12 | Sequence 12, Appl1 |
| 41 | 699.5 | 26.2 | 536 | US-08-232-545-12 | Sequence 12, Appl1 |
| 42 | 699.5 | 26.2 | 536 | PCR-US95-05008-12 | Sequence 12, Appl1 |
| 43 | 699 | 26.2 | 499 | US-08-426-509A-19 | Sequence 19, Appl1 |
| 44 | 699 | 26.2 | 499 | US-08-232-545-19 | Sequence 19, Appl1 |
| 45 | 699 | 26.2 | 499 | PCR-US95-05008-19 | Sequence 19, Appl1 |

ALIGNMENTS

RESULT 1
US-08-426-509A-2
; Sequence 2, Application US/08426509A
; Patent No. 6326469
; GENERAL INFORMATION:
; APPLICANT: Gishlitzky, Axel
; APPLICANT: Sures, Irman G.
; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN
; TITLE OF INVENTION: TYROSINE KINASES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York,
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/426,509A
; FILING DATE: 21-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/232,545
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 7683-0074-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 507 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: NO. 6326469e
; US-08-426-509A-2
Query Match 100.0%; Score 2671; DB 4; Length 507;
Best Local Similarity 100.0%; Pred. No. 2.7e-219;
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MAGGSLVSWRAFHGCDASAEELPRVSPRLRAHMPPVVSARMPTRRAAPGTCITKCEHT 60
D 1 MAGGSLVSWRAFHGCDASAEELPRVSPRLRAHMPPVVSARMPTRRAAPGTCITKCEHT 60
QY 61 RPKRGELAFRRKGDVYTLLEACENKSWYRVKHHHTSGOGLLAAGALRREALSADPKLSLM 120
D 61 RPKRGELAFRRKGDVYTLLEACENKSWYRVKHHHTSGOGLLAAGALRREALSADPKLSLM 120
QY 121 PWFHKGKISGQEAQQQLPPEDGFLVRESARHGGDYVLCVSGRDVYHYRVLHRDGHLLTI 180
D 121 PWFHKGKISGQEAQQQLPPEDGFLVRESARHGGDYVLCVSGRDVYHYRVLHRDGHLLTI 180
QY 181 DEAVFPCNLMDMVEHYSKDGAICTKLVPRKRKHGTSABEELARAGMLNLQHLTLGAQ 240
D 181 DEAVFPCNLMDMVEHYSKDGAICTKLVPRKRKHGTSABEELARAGMLNLQHLTLGAQ 240
QY 241 IGESEFGAVLQGEYLQGVAVKNIKCDVTAQAFLEDTAVMTKQHENLVLLGVYLLHQL 300
D 241 IGESEFGAVLQGEYLQGVAVKNIKCDVTAQAFLEDTAVMTKQHENLVLLGVYLLHQL 300
QY 301 YIYVEHYSKGNLVNLTFRGRALVNTAQLQFSLHVAEGMEYLESKKLVHRDLAARNILV 360
D 301 YIYVEHYSKGNLVNLTFRGRALVNTAQLQFSLHVAEGMEYLESKKLVHRDLAARNILV 360
QY 361 SEDLVAKVSDFGGLAKARERKGLDSSRLPVKWTAPALKHGKFTSKSDVMSFGVLLMEVFSY 420
D 361 SEDLVAKVSDFGGLAKARERKGLDSSRLPVKWTAPALKHGKFTSKSDVMSFGVLLMEVFSY 420
QY 421 GRAPYPMKSLKEYSEAVEKGYRMEPPGCGPVHYVLMSSCWEAPARPPFRKLAELAR 480
D 421 GRAPYPMKSLKEYSEAVEKGYRMEPPGCGPVHYVLMSSCWEAPARPPFRKLAELAR 480
QY 481 ELRSAGAPASVSGODADGTSPPRSQEP 507
D 481 ELRSAGAPASVSGODADGTSPPRSQEP 507

RESULT 2
US-08-232-545-2
: Sequence 2, Application US/08232545
: Patent No. 6506578
: GENERAL INFORMATION:
: APPLICANT: Ullrich, Axel
: APPLICANT: Gishizsky, Mikhail
: APPLICANT: Sures, Irmann G.
: TITLE OF INVENTION: No. 6506578el Megakaryocytic Protein Tyrosine
: TITLE OF INVENTION: Kinases
: NUMBER OF SEQUENCES: 21
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennile & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/232,545
: FILING DATE: 22-APR-1994
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Cotuzzi, Laura A.
: REGISTRATION NUMBER: 30,742
: REFERENCE/DOCKET NUMBER: 7683-050
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212)790-9090
: TELEFAX: (212)869-9741
: TELEX: 66141 PENNIE

```

```

: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 507 amino acids
: TYPE: amino acid
: STRANDEDNESS: unknown
: TOPOLOGY: unknown
: MOLECULE TYPE: protein
: US-08-232-545-2

Query Match      100.0%; Score 2671; DB 4; Length 507;
Best Local Similarity 100.0%; Pred. No. 2.7e-219;
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGGSLVSWRAFHGCDASAEELPRVSPRLRAHMPPVVSARMPTRRAAPGTCITKCEHT 60
D 1 MAGGSLVSWRAFHGCDASAEELPRVSPRLRAHMPPVVSARMPTRRAAPGTCITKCEHT 60
QY 61 RPKRGELAFRRKGDVYTLLEACENKSWYRVKHHHTSGOGLLAAGALRREALSADPKLSLM 120
D 61 RPKRGELAFRRKGDVYTLLEACENKSWYRVKHHHTSGOGLLAAGALRREALSADPKLSLM 120
QY 121 PWFHKGKISGQEAQQQLPPEDGFLVRESARHGGDYVLCVSGRDVYHYRVLHRDGHLLTI 180
D 121 PWFHKGKISGQEAQQQLPPEDGFLVRESARHGGDYVLCVSGRDVYHYRVLHRDGHLLTI 180
QY 181 DEAVFPCNLMDMVEHYSKDGAICTKLVPRKRKHGTSABEELARAGMLNLQHLTLGAQ 240
D 181 DEAVFPCNLMDMVEHYSKDGAICTKLVPRKRKHGTSABEELARAGMLNLQHLTLGAQ 240
QY 241 IGESEFGAVLQGEYLQGVAVKNIKCDVTAQAFLEDTAVMTKQHENLVLLGVYLLHQL 300
D 241 IGESEFGAVLQGEYLQGVAVKNIKCDVTAQAFLEDTAVMTKQHENLVLLGVYLLHQL 300
QY 301 YIYVEHYSKGNLVNLTFRGRALVNTAQLQFSLHVAEGMEYLESKKLVHRDLAARNILV 360
D 301 YIYVEHYSKGNLVNLTFRGRALVNTAQLQFSLHVAEGMEYLESKKLVHRDLAARNILV 360
QY 361 SEDLVAKVSDFGGLAKARERKGLDSSRLPVKWTAPALKHGKFTSKSDVMSFGVLLMEVFSY 420
D 361 SEDLVAKVSDFGGLAKARERKGLDSSRLPVKWTAPALKHGKFTSKSDVMSFGVLLMEVFSY 420
QY 421 GRAPYPMKSLKEYSEAVEKGYRMEPPGCGPVHYVLMSSCWEAPARPPFRKLAELAR 480
D 421 GRAPYPMKSLKEYSEAVEKGYRMEPPGCGPVHYVLMSSCWEAPARPPFRKLAELAR 480
QY 481 ELRSAGAPASVSGODADGTSPPRSQEP 507
D 481 ELRSAGAPASVSGODADGTSPPRSQEP 507

RESULT 3
PCT-US95-05008-2
: Sequence 2, Application PC/TUS9505008
: GENERAL INFORMATION:
: APPLICANT: Sugen, Inc.
: APPLICANT: 515 Galveston Drive
: APPLICANT: Redwood City, California 94063-4720
: APPLICANT: United States of America
: APPLICANT: Wissenschaften E.V.
: APPLICANT: Horigarten Str. 2
: APPLICANT: Munchen 80539
: APPLICANT: Germany
: TITLE OF INVENTION: Novel Megakaryocytic Protein Tyrosine
: TITLE OF INVENTION: Kinases
: NUMBER OF SEQUENCES: 21
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennile & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036
: COMPUTER READABLE FORM:

```

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05008
CLASSIFICATION:
FILING DATE: 24-APR-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/232,545
FILING DATE: 22-APR-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-074
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEFAX: (212)869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 507 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
PCT-US95-05008-2

Query Match 100.0%; Score 2671; DB 5; Length 507;
Best Local Similarity 100.0%; Pred. No. 2.7e-219;
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGRGSLSVSRARHGCDSAEELPRVSPRFLRAWHPPVVSARMPTRRAPGTCTTKEHT 60
DB 1 MAGRGSLSVSRARHGCDSAEELPRVSPRFLRAWHPPVVSARMPTRRAPGTCTTKEHT 60
QY 61 RPKPGEIAPFRKGDVVTILEACENKSWRVKHNHTSGOGLLAAGALRREALSADPKISLM 120
DB 61 RPKPGEIAPFRKGDVVTILEACENKSWRVKHNHTSGOGLLAAGALRREALSADPKISLM 120
QY 121 PWFHKGISGQEAVALQPPEDGFLVRESARHPGDVYLCVSGRDVHYRYLHRDGLTI 180
DB 121 PWFHKGISGQEAVALQPPEDGFLVRESARHPGDVYLCVSGRDVHYRYLHRDGLTI 180
QY 181 DEAVFPCNLDMDVHEHYSKDKGALCTKLVPRKRHGTSAEELARAGWMLNLOHLTLGAO 240
DB 181 DEAVFPCNLDMDVHEHYSKDKGALCTKLVPRKRHGTSAEELARAGWMLNLOHLTLGAO 240
QY 241 IGESEGAVALQGEYLGOKVAVKNIKCDVTAQAFLEDTAVMTKMOHENLVRLGLVILHOG 300
DB 241 IGESEGAVALQGEYLGOKVAVKNIKCDVTAQAFLEDTAVMTKMOHENLVRLGLVILHOG 300
QY 301 YIYMEHVSCKNLVNFLETRGRALVNTAQLQFSLHVAEGMEYLESKKLVHRDLAARNILV 360
DB 301 YIYMEHVSCKNLVNFLETRGRALVNTAQLQFSLHVAEGMEYLESKKLVHRDLAARNILV 360
QY 361 SEDLVAKVSDPFGAKARERKLDSSRLPVKWTAPALKHGFTSKSDVWSGVLMEVFSY 420
DB 361 SEDLVAKVSDPFGAKARERKLDSSRLPVKWTAPALKHGFTSKSDVWSGVLMEVFSY 420
QY 421 GRAPYPMSLKEVSEAEVKEGYRMEPPGCGPVPVHLMSCWEAEPARPPFRKLAETLAR 480
DB 421 GRAPYPMSLKEVSEAEVKEGYRMEPPGCGPVPVHLMSCWEAEPARPPFRKLAETLAR 480
QY 481 ELRSAGAPASVSGODADGSTSPRSQEP 507
DB 481 ELRSAGAPASVSGODADGSTSPRSQEP 507

RESULT 4
US-08-604-989A-5
; Sequence 5, Application US/08604989A

Patent No. 5834208
GENERAL INFORMATION:
APPLICANT: Sakano, S.
TITLE OF INVENTION: NO. 5834208el Tyrosine Kinase
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/604,989A
FILING DATE: February 23, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Charles E. Miller
REGISTRATION NUMBER: 24,576
REFERENCE/DOCKET NUMBER: 1920-026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 507 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: human
STRAIN: UT-7
US-08-604-989A-5

Query Match 99.7%; Score 2664; DB 2; Length 507;
Best Local Similarity 99.8%; Pred. No. 1e-218;
Matches 506; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAGRGSLSVSRARHGCDSAEELPRVSPRFLRAWHPPVVSARMPTRRAPGTCTTKEHT 60
DB 1 MAGRGSLSVSRARHGCDSAEELPRVSPRFLRAWHPPVVSARMPTRRAPGTCTTKEHT 60
QY 61 RPKPGEIAPFRKGDVVTILEACENKSWRVKHNHTSGOGLLAAGALRREALSADPKISLM 120
DB 61 RPKPGEIAPFRKGDVVTILEACENKSWRVKHNHTSGOGLLAAGALRREALSADPKISLM 120
QY 121 PWFHKGISGQEAVALQPPEDGFLVRESARHPGDVYLCVSGRDVHYRYLHRDGLTI 180
DB 121 PWFHKGISGQEAVALQPPEDGFLVRESARHPGDVYLCVSGRDVHYRYLHRDGLTI 180
QY 181 DEAVFPCNLDMDVHEHYSKDKGALCTKLVPRKRHGTSAEELARAGWMLNLOHLTLGAO 240
DB 181 DEAVFPCNLDMDVHEHYSKDKGALCTKLVPRKRHGTSAEELARAGWMLNLOHLTLGAO 240
QY 241 IGESEGAVALQGEYLGOKVAVKNIKCDVTAQAFLEDTAVMTKMOHENLVRLGLVILHOG 300
DB 241 IGESEGAVALQGEYLGOKVAVKNIKCDVTAQAFLEDTAVMTKMOHENLVRLGLVILHOG 300
QY 301 YIYMEHVSCKNLVNFLETRGRALVNTAQLQFSLHVAEGMEYLESKKLVHRDLAARNILV 360
DB 301 YIYMEHVSCKNLVNFLETRGRALVNTAQLQFSLHVAEGMEYLESKKLVHRDLAARNILV 360
QY 361 SEDLVAKVSDPFGAKARERKLDSSRLPVKWTAPALKHGFTSKSDVWSGVLMEVFSY 420
DB 361 SEDLVAKVSDPFGAKARERKLDSSRLPVKWTAPALKHGFTSKSDVWSGVLMEVFSY 420
QY 421 GRAPYPMSLKEVSEAEVKEGYRMEPPGCGPVPVHLMSCWEAEPARPPFRKLAETLAR 480
DB 421 GRAPYPMSLKEVSEAEVKEGYRMEPPGCGPVPVHLMSCWEAEPARPPFRKLAETLAR 480

Db 421 GRAPYKMSLKEVSEAVEKGYRMEPEGCPGVHVLMSCEWAEAPRRPFRLAEKLAR 480
QY 481 ELRSAGAPASVSGODADGSTSPRSQ 507
Db 481 ELRSAGAPASVSGODADGSTSPRSQ 507

RESULT 5

US-09-315-928-2
; Sequence 2, Application US/09315928
; Patent No. 6368796
; GENERAL INFORMATION:
; APPLICANT: Groopman, Jerome E.
; TITLE OF INVENTION: METHODS OF DETECTION AND TREATMENT OF
; FILE REFERENCE: MED97-01PAZ
; CURRENT APPLICATION NUMBER: US/09/315,928
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: US 08/876,882
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 60/035,228
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 527
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-315-928-2

Query Match 91.5%; Score 2445; DB 4; Length 527;
Best Local Similarity 93.5%; Pred. No. 4.9e-200;
Matches 472; Conservative 1; Mismatches 18; Indels 14; Gaps 2;

QY 1 MAGRGSVSWRAFHGCDSEELPRVSPRLRAMHPPVSARMPTRRMAGTCTKCEHT 60
Db 1 MAGRGSVSWRAFHGCDSEELPRVSPRLRAMHPPVSARMPTRRMAGTCTKCEHT 60
QY 61 RPKPGELARKGDDVITLACENKSWYRKHNHSGOGLLAGALREBRLSADPKLSLM 120
Db 61 RPKPGELARKGDDVITLACENKSWYRKHNHSGOGLLAGALREBRLSADPKLSLM 120
QY 121 PMFHGKISGOEAVOQLOPPEDGLFLVRESARHPGDIVLCVSGRDVIYHRLVLRDGLTI 180
Db 121 PMFHGKISGOEAVOQLOPPEDGLFLVRESARHPGDIVLCVSGRDVIYHRLVLRDGLTI 180
QY 181 DEAVFPCLMDVNEHYSKDKGAICTKLVRPKRHGKTSABEELARAGWLLNLOHTLGAQ 240
Db 181 DEAVFPCLMDVNEHYSKDKGAICTKLVRPKRHGKTSABEELARAGWLLNLOHTLGAQ 240
QY 241 ISEGEFVAVLGEYIGOKAVVKNICDVTAAFLDETAVMTKMOHNLVRLIGVILHOGI 300
Db 241 ISEGEFVAVLGEYIGOKAVVKNICDVTAAFLDETAVMTKMOHNLVRLIGVILHOGI 300
QY 301 YVMEHVSNGNLVNLRTGRALVNTAQLLOFSLHVAEGMEYLESKKLVHRDLAANILY 360
Db 301 YVMEHVSNGNLVNLRTGRALVNTAQLLOFSLHVAEGMEYLESKKLVHRDLAANILY 360
QY 361 SEDLVAKVSDPGLAKAERKGLDSSRLPVKWTAPALKHGKFTSKSDVMSFGVILMEVFSY 420
Db 361 SEDLVAKVSDPGLAKAERKGLDSSRLPVKWTAPALKHGKFTSKSDVMSFGVILMEVFSY 420
QY 421 GRAPYKMSLKEVSEAVEKGYRMEPEGCPGVHVLMSCEWAEAPRRPFRLAEKLAR 480
Db 421 GRAPYKMSLKEVSEAVEKGYRMEPEGCPGVHVLMSCEWAEAPRRPFRLAEKLAR 480
QY 481 ELRSAGAPASVSGODADGSTSPRSQ 505
Db 481 ELRSAGAPASVSGODADGSTSPRSQ 505
QY 470 ---SANNPRSMGSGYAVOYPPPSQ 491
Db 470 ---SANNPRSMGSGYAVOYPPPSQ 491

RESULT 6

US-08-604-989A-4
; Sequence 4, Application US/08604989A
; Patent No. 5834208
; GENERAL INFORMATION:
; APPLICANT: Sakano, S.
; TITLE OF INVENTION: No. 5834208el Tyrosine Kinase
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/604,989A
; FILING DATE: February 23, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles E. Miller
; REGISTRATION NUMBER: 24,576
; REFERENCE/DOCKET NUMBER: 1920-026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 869-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 466 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: human
; STRAIN: UT-7
US-08-604-989A-4

Query Match 91.5%; Score 2444; DB 2; Length 466;
Best Local Similarity 100.0%; Pred. No. 5e-200;
Matches 466; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 MPTRRMAGTCTKCEHTRPKPGELARKGDDVITLACENKSWYRKHNHSGOGLLA 101
Db 42 MPTRRMAGTCTKCEHTRPKPGELARKGDDVITLACENKSWYRKHNHSGOGLLA 101
QY 102 AGALRREALSADPKLSLMPFHGKISGOEAVOQLOPPEDGLFLVRESARHPGDIVLCV 161
Db 102 AGALRREALSADPKLSLMPFHGKISGOEAVOQLOPPEDGLFLVRESARHPGDIVLCV 161
QY 162 FGRDVIHVRVLRDGLTIIDEAVFPCLMDVNEHYSKDKGAICTKLVRPKRHGKTSABE 221
Db 162 FGRDVIHVRVLRDGLTIIDEAVFPCLMDVNEHYSKDKGAICTKLVRPKRHGKTSABE 221
QY 222 ELARAGWLLNLOHTLGAOIGGEFVAVLGEYIGOKAVVKNICDVTAAFLDETAVMT 281
Db 222 ELARAGWLLNLOHTLGAOIGGEFVAVLGEYIGOKAVVKNICDVTAAFLDETAVMT 281
QY 282 KMÖHENVLLGVILHOGIYVMEHVSNGNLVNLRTGRALVNTAQLLOFSLHVAEGME 341
Db 282 KMÖHENVLLGVILHOGIYVMEHVSNGNLVNLRTGRALVNTAQLLOFSLHVAEGME 341
QY 342 YLESKLVHRDLAANILVSEDLVAKVSDPGLAKAERKGLDSSRLPVKWTAPALKHGKF 401
Db 342 YLESKLVHRDLAANILVSEDLVAKVSDPGLAKAERKGLDSSRLPVKWTAPALKHGKF 401
QY 402 TSKSDVMSFGVILMEVFSYGRAPYKMSLKEVSEAVEKGYRMEPEGCPGVHVLMSCEW 461
Db 402 TSKSDVMSFGVILMEVFSYGRAPYKMSLKEVSEAVEKGYRMEPEGCPGVHVLMSCEW 461

Db 361 TSKSDVMSFGVLLMEVFSYGRAPYPKMSLKEVSEAVEKGRMEPECCPGPVHVLMSWCW 420
QY 462 EAEPRARPPRKLAEKLAELRSAGAPASVSGODADSTSPRSOEP 507
Db 421 EAEPRARPPRKLAEKLAELRSAGAPASVSGODADSTSPRSOEP 466

RESULT 7

US-08-876-882-2
Sequence 2, Application US/08876882
Patent No. 5981201
GENERAL INFORMATION:
APPLICANT: Avraham, Hava
APPLICANT: Groopman, Jerome E.
TITLE OF INVENTION: METHODS OF DETECTION AND TREATMENT
TITLE OF INVENTION: OF BREAST CANCER
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds P.C.
STREET: Two Miltia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: WINDOWS
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/876, 882
FILING DATE: 16-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/035, 228
FILING DATE: 08-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Doreen, Hogle M
REGISTRATION NUMBER: 36,361
REFERENCE/DOCKET NUMBER: NEDH97-01PA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 528 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-876-882-2

Query Match 91.1%; Score 2434.5; DB 2; Length 528;
Best Local Similarity 93.3%; Pred. No. 3.8e-199;
Matches 472; Conservative 1; Mismatches 18; Indels 15; Gaps 3;

QY 1 MAGGSLVSWRAHFGCSAEELPRVSPRLRAMHPVVSARMPRRRPAFGTCTTCKEHT 60
Db 1 MAGGSLVSWRAHFGCSAEELPRVSPRLRAMHPVVSARMPRRRPAFGTCTTCKEHT 60
QY 61 RPRKGEIAFRKGDVVTI-LEACEKSMYRYKHHHTSGOGLLAAGALRERALSADPKLSL 119
Db 61 RPRKGEIAFRKGDVVTI-LEACEKSMYRYKHHHTSGOGLLAAGALRERALSADPKLSL 120
QY 120 MPWFHGRISGOEAVQOLQPPEDGLFLVRESARHPGDVLCVSGRDVIHYRVHLRDGHLT 179
Db 121 MPWFHGRISGOEAVQOLQPPEDGLFLVRESARHPGDVLCVSGRDVIHYRVHLRDGHLT 180
QY 180 IDEAVFFCNLMDMVEHYSKDKGAICTKLVPRKRGKHSAAEELARAGMLNLOHLLTGA 239
Db 181 IDEAVFFCNLMDMVEHYSKDKGAICTKLVPRKRGKHSAAEELARAGMLNLOHLLTGA 240

QY 240 QIGEGEAGVLOGEYLQOKAVVKNIKCDVTAQAELEDTAVMTKMQHENLVRLGLVILHOG 299
Db 241 QIGEGEAGVLOGEYLQOKAVVKNIKCDVTAQAELEDTAVMTKMQHENLVRLGLVILHOG 300
QY 300 LYIVMEHVSNGNLVNLRTGRALVNTAQLQFSLVHAEGBMEYLESKKLVHRDLAARNIL 359
Db 301 LYIVMEHVSNGNLVNLRTGRALVNTAQLQFSLVHAEGBMEYLESKKLVHRDLAARNIL 360
QY 360 VSEDVAKVSDPGLAKKERKGLDSSRLPVKWTAPALKHGFTSKSDVMSFGVLLMEVFSY 419
Db 361 VSEDVAKVSDPGLAKKERKGLDSSRLPVKWTAPALKHGFTSKSDVMSFGVLLMEVFSY 419
QY 420 YGRAPYPKMSLKEVSEAVEKGRMEPECCPGPVHVLMSGCWEAEAPARPPRKLAEKLA 479
Db 420 YGRAPYPKMSLKEVSEAVEKGRMEPECCPGPVHVLMSGCWEAEAPARPPRKLAEKLA 479
QY 480 RELRSAGAPASVSGODADSTSPRSQ 505
Db 471 ----SAMPWRSPGSAVAVQVPQPSQ 492

RESULT 8

US-09-741-154-4
Sequence 4, Application US/09741154
Patent No. 6437110
GENERAL INFORMATION:
APPLICANT: BEASLEY, Ellen M. et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
FILE REFERENCE: CLO01061
CURRENT APPLICATION NUMBER: US/09/741,154
CURRENT FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 386
TYPE: PRT
ORGANISM: Human
US-09-741-154-4

Query Match 75.3%; Score 1012; DB 4; Length 386;
Best Local Similarity 100.0%; Pred. No. 2.4e-163;
Matches 386; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 122 WFHGRISGOEAVQOLQPPEDGLFLVRESARHPGDVLCVSGRDVIHYRVHLRDGHLTID 181
Db 1 WFHGRISGOEAVQOLQPPEDGLFLVRESARHPGDVLCVSGRDVIHYRVHLRDGHLTID 181
QY 182 EAEVFCNLMDMVEHYSKDKGAICTKLVPRKRGKHSAAEELARAGMLNLOHLLTGAOI 241
Db 61 EAEVFCNLMDMVEHYSKDKGAICTKLVPRKRGKHSAAEELARAGMLNLOHLLTGAOI 120
QY 242 GEGEFGAVLOGEYLQOKAVVKNIKCDVTAQAELEDTAVMTKMQHENLVRLGLVILHOG 301
Db 121 GEGEFGAVLOGEYLQOKAVVKNIKCDVTAQAELEDTAVMTKMQHENLVRLGLVILHOG 180
QY 302 LYIVMEHVSNGNLVNLRTGRALVNTAQLQFSLVHAEGBMEYLESKKLVHRDLAARNIL 361
Db 181 LYIVMEHVSNGNLVNLRTGRALVNTAQLQFSLVHAEGBMEYLESKKLVHRDLAARNIL 240
QY 362 EDVAKVSDPGLAKKERKGLDSSRLPVKWTAPALKHGFTSKSDVMSFGVLLMEVFSY 421
Db 241 EDVAKVSDPGLAKKERKGLDSSRLPVKWTAPALKHGFTSKSDVMSFGVLLMEVFSY 300
QY 422 RAPPYKMSLKEVSEAVEKGRMEPECCPGPVHVLMSGCWEAEAPARPPRKLAEKLA 481
Db 301 RAPPYKMSLKEVSEAVEKGRMEPECCPGPVHVLMSGCWEAEAPARPPRKLAEKLA 360
QY 482 LRSAGAPASVSGODADSTSPRSOEP 507
Db 361 LRSAGAPASVSGODADSTSPRSOEP 386

RESULT 9
US-09-741-154-2
; Sequence 2, Application US/09741154
; Patent No. 6437110
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen M. et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001061
; CURRENT APPLICATION NUMBER: US/09/741,154
; CURRENT FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 415
; TYPE: PR1
; ORGANISM: Human
US-09-741-154-2

Query Match 75.3%; Score 2012; DB 4; Length 415;
Best Local Similarity 100.0%; Pred. No. 2,6e-163;
Matches 386; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 122 MFHGKISGGEAVQQLPPEDGFLVRESARHPDGYLCVSGFDVHYHYRLHRDGLTID 181
DB 30 MFHGKISGGEAVQQLPPEDGFLVRESARHPDGYLCVSGFDVHYHYRLHRDGLTID 89
QY 182 EAFPCNLMVMHYHYSKDKAICTKLYPRKRHGTSAEELARAGMLNLQHLTGAQI 241
DB 90 EAFPCNLMVMHYHYSKDKAICTKLYPRKRHGTSAEELARAGMLNLQHLTGAQI 149
QY 242 GEGEFGAVLQGEYLGQKVAANKICDVTQAFLDETAVMTKMOHENVRLGLYILHOGLY 301
DB 150 GEGEFGAVLQGEYLGQKVAANKICDVTQAFLDETAVMTKMOHENVRLGLYILHOGLY 209
QY 302 IYMEHVSQGNLVNLTGRALVNTAQLQFSLHVAEGMEYLSKKLVHRDLAARNILVS 361
DB 210 IYMEHVSQGNLVNLTGRALVNTAQLQFSLHVAEGMEYLSKKLVHRDLAARNILVS 269
QY 362 EDIVAVSDPGLAKARKKGLDSSRLPYKWTAPALKHGKTSKSDVWSFVLLMEVFSYG 421
DB 270 EDIVAVSDPGLAKARKKGLDSSRLPYKWTAPALKHGKTSKSDVWSFVLLMEVFSYG 329
QY 422 RAPIPKMSLKEVSEAVEKGYRMPPEGCPGVHVLMSSCWEAPARPPRKLAEKLARE 481
DB 330 RAPIPKMSLKEVSEAVEKGYRMPPEGCPGVHVLMSSCWEAPARPPRKLAEKLARE 389
QY 482 LRSAGAPASVSGODADGSTSIPRSQEP 507
DB 390 LRSAGAPASVSGODADGSTSIPRSQEP 415

RESULT 10
US-08-604-989A-3
; Sequence 3, Application US/08604989A
; Patent No. 5834208
; GENERAL INFORMATION:
; APPLICANT: Sakano, S.
; TITLE OF INVENTION: No. 5834208el Tyrosine kinase
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/604,989A
FILING DATE: February 23, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Charles E. Miller
REGISTRATION NUMBER: 24,576
REFERENCE/DOCKET NUMBER: 1920-026
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 246 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: human
STRAIN: UT-7
US-08-604-989A-3

Query Match 47.5%; Score 1269; DB 2; Length 246;
Best Local Similarity 100.0%; Pred. No. 2,4e-100;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 233 OHLTGAQIGEGEFGVILQGEYLGQKVAANKICDVTQAFLDETAVMTKMOHENVRL 292
DB 1 OHLTGAQIGEGEFGVILQGEYLGQKVAANKICDVTQAFLDETAVMTKMOHENVRL 60
QY 293 GVILHOGLYIYMEHVSQGNLVNLTGRALVNTAQLQFSLHVAEGMEYLSKKLVHRD 352
DB 61 GVILHOGLYIYMEHVSQGNLVNLTGRALVNTAQLQFSLHVAEGMEYLSKKLVHRD 120
QY 353 LAARNILVSEBDLVAKVSDPGLAKARKKGLDSSRLPYKWTAPALKHGKTSKSDVWSFV 412
DB 121 LAARNILVSEBDLVAKVSDPGLAKARKKGLDSSRLPYKWTAPALKHGKTSKSDVWSFV 180
QY 413 LMEVFSYGRAPPKMSLKEVSEAVEKGYRMPPEGCPGVHVLMSSCWEAPARPPR 472
DB 181 LMEVFSYGRAPPKMSLKEVSEAVEKGYRMPPEGCPGVHVLMSSCWEAPARPPR 240
QY 473 KLAEKL 478
DB 241 KLAEKL 246

RESULT 11
US-08-426-509A-7
; Sequence 7, Application US/08426509A
; Patent No. 6326469
; GENERAL INFORMATION:
; APPLICANT: Ulitich, Axel
; APPLICANT: Gishizky, Mikhail
; APPLICANT: Sures, Irman G.
; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN
; TITLE OF INVENTION: TYROSINE KINASES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:

ADDRESSEE: Pennie & Edmonds

; GENERAL INFORMATION:
ADDICAVE: CUSTO THE

Db 121 METLEENNVHDIILAAINLVSESDVAVKSYDGLTKKASSPQDQGIKLPVKMTAPEALREK 180

QY 400 KFTSKSDVMSFGVLLMEVEFSYGRAPYPMKSLKEVSEAVEKGYRMEPEGCGPAPHVLMSS 459

Dd 181 KFTSKSDVMSFGVLLMEIYSFGRVYPRIPLKDVYPRKEKQKMDADGCGPRATVEYMKN 240

QY 460 CMEAEPRARPPRKLAEKL 478

Dd 241 CMHLDAMRPSFLQLEQL 259

RESULT 15
US-09-035-706-3

1 PATENT NO. 6001622
 2 GENERAL INFORMATION:
 3 APPLICANT: Dedhar, Shoukat
 4 APPLICANT: Hannigan, Greg
 5 TITLE OF INVENTION: Integrin-Linked Kinase and
 6 TITLE OF INVENTION: Its Uses
 7 NUMBER OF SEQUENCES: 11
 8 CORRESPONDENCE ADDRESS:
 9 ADDRESSEE: Bozicevic & Reed, LLP
 10 STREET: 285 Hamilton Avenue, Suite 200
 11 CITY: Palo Alto
 12 STATE: CA
 13 COUNTRY: USA
 14 ZIP: 94301
 15 COMPUTER READABLE FORM:
 16 MEDIUM TYPE: Diskette
 17 COMPUTER: IBM Compatible
 18 OPERATING SYSTEM: DOS
 19 SOFTWARE: FASTSEQ for Windows Version 2.0
 20 CURRENT APPLICATION DATA:
 21 APPLICATION NUMBER: US/09/035.706
 22 FILING DATE:
 23 CLASSIFICATION:
 24 PRIOR APPLICATION DATA:
 25 APPLICATION NUMBER:
 26 FILING DATE:
 27 ATTORNEY/AGENT INFORMATION:
 28 NAME: Sherwood, Pamela J
 29 REGISTRATION NUMBER: 36,677
 30 REFERENCE/DOCKET NUMBER: KIN-2C1P1
 31 TELECOMMUNICATION INFORMATION:
 32 TELEPHONE: 650-327-3400
 33 TELEFAX: 650 327-3231
 34 TELETEX:
 35 INFORMATION FOR SEQ ID NO: 3:
 36 SEQUENCE CHARACTERISTICS:
 37 LENGTH: 258 amino acids
 38 TYPE: amino acid
 39 STRANDEDNESS: single
 40 TOPOLOGY: linear
 41 MOLECULE TYPE: protein
 42 OS-09-035-706-3

| | | | | |
|-----------------------|-----------------|-------------------|----------|------------|
| Query Match | 28.8% | Score 768 | DB 3 | Length 258 |
| Best Local Similarity | 58.8% | Pred. NO. 1.2e-57 | | |
| Matches 147 | Conservative 45 | Mismatches 56 | Indels 2 | Gaps 1 |

| | | | |
|----|-----|--|-----|
| QY | 231 | NIQHLLTGAQIGDEEFGVILQGEYLGGKVAAYKNIKCDVTAQAFLEDETANVTMTQMHENLVR | 290 |
| | | : : : : : : : : : : : : : : : : : : | |
| Db | 1 | NMKLTKLLQTTIGKKEFGDVMILG DYRGKNGVAAYCKIKNDATAAQAFLEAASVYPTDILRHSNIQ | 60 |
| QY | 291 | LLGVITLHO--GLIYVMEHVSKGNLYNFIKRTGRBALVYNAQLLOFSLHVAEGMEYTESEKTL | 348 |
| | | : : : : : : : : : : : : : : : : : : | |
| Db | 61 | LLGVIVVEKGGLIYVTEYMAKGSGLVDYIRSRORSVGLGDCILKTFSLDVC EAENYELEGNNF | 120 |
| QY | 349 | VHRIILARNIIVSEDIYAKVSDFGLAKAEKRGIDSSRLPVKWTAPAEALHKGKFTSKSDWA | 408 |
| | | : : : : : : : : : : : : : : : : : : | |
| Db | 121 | VHRIILARNIIVSEDIYAKVSDFGLTKAASSTQDYGKLPVKWTAPAEALKEKFTSKSDWA | 180 |

| | | | |
|----|-----|---|-----|
| Oy | 409 | SEGLLLEWVSYSTRAPYPMKSLKEVSEAVERKCGRPYHVLMSCEADARR | 468 |
| | | : : : : : : : : : : : | |
| Dd | 181 | SFGLIMEIYSFCRVRYPRIPLKDVPRVEKKYKMDADPGCPRAVYEVMKKMCHLDAMR | 240 |
| Oy | 469 | PPPKLAERKL 478 | |
| | | : : : | |
| Dd | 241 | PSELQREQL 250 | |

Search completed: July 29, 2003, 09:52:34
Job time : 22 secs

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OM protein - protein search, using sw model

Run on: July 29, 2003, 09:46:12 ; Search time 44 Seconds

(without alignments)
1828.963 Million cell updates/sec

Title: US-09-977-261-2

Perfect score: 2671

Sequence: 1 MAGRSLVSMRAFHCDSAE.....PASVSGDADGSTRPSRQEP 507

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: A_Geneseq-19Jun03:*
2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
4: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
5: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
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9: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
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22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
25: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|--------|---------------------|
| 1 | 2671 | 100.0 | 507 | AA1980 | Cytoplasmic tyrosin |
| 2 | 2671 | 100.0 | 507 | AA1981 | Human mark-related |
| 3 | 2668 | 99.9 | 507 | AA1982 | Megakaryocyte kina |
| 4 | 2444 | 91.5 | 466 | AA1983 | N-terminal truncat |
| 5 | 2434.5 | 91.1 | 528 | AA1984 | Human mark protein |
| 6 | 2012 | 75.3 | 415 | AA1985 | Human kinase relat |
| 7 | 1261 | 47.2 | 246 | AA1986 | Tyrosine kinase do |
| 8 | 1247.5 | 46.7 | 459 | AA1987 | Human polypeptide |
| 9 | 1245.5 | 46.6 | 450 | AA1988 | Wild-type human c- |

| | | | | | |
|----|--------|------|------|--------|---------------------|
| 10 | 1245.5 | 46.6 | 450 | AA1989 | PKA substrate, Csk |
| 11 | 1245.5 | 46.6 | 450 | AA1990 | Amino acid sequenc |
| 12 | 1245.5 | 46.6 | 450 | AA1991 | Amino acid sequenc |
| 13 | 1245.5 | 46.6 | 450 | AA1992 | Amino acid sequenc |
| 14 | 1245.5 | 46.6 | 450 | AA1993 | Breast cancer asso |
| 15 | 979.5 | 36.7 | 820 | AA1994 | Drosophila melanog |
| 16 | 916 | 34.3 | 357 | AA1995 | Human SH2/SH3 doma |
| 17 | 753 | 28.2 | 502 | AA1996 | Fugu rubripes lymph |
| 18 | 745 | 27.9 | 567 | AA1997 | Tumour involved ge |
| 19 | 742.5 | 27.8 | 508 | AA1998 | Human lymphocyte k |
| 20 | 736.5 | 27.6 | 509 | AA1999 | PKA substrate, Src |
| 21 | 735 | 27.5 | 533 | AA2000 | Chicken pp60 c-src |
| 22 | 733 | 27.4 | 533 | AA2001 | Wild-type chicken |
| 23 | 733 | 27.4 | 533 | AA2002 | Mutant chicken c-S |
| 24 | 733 | 27.4 | 533 | AA2003 | Amino acid sequenc |
| 25 | 727 | 27.2 | 533 | AA2004 | Mutant chicken c-S |
| 26 | 727 | 27.2 | 536 | AA2005 | Human pp60 c-src p |
| 27 | 727 | 27.2 | 536 | AA2006 | Human v-src isoform |
| 28 | 727 | 27.2 | 536 | AA2007 | Human SH2/SH3 doma |
| 29 | 727 | 27.2 | 536 | AA2008 | Human src-c protei |
| 30 | 724 | 27.1 | 1504 | AA2009 | Drosophila melanog |
| 31 | 720.5 | 27.0 | 505 | AA2010 | Human tyrosine kin |
| 32 | 718 | 26.9 | 542 | AA2011 | Novel human protei |
| 33 | 714 | 26.7 | 541 | AA2012 | Mouse src-c protei |
| 34 | 710 | 26.6 | 543 | AA2013 | Novel human diagno |
| 35 | 710 | 26.6 | 543 | AA2014 | Amino acid sequenc |
| 36 | 708 | 26.5 | 541 | AA2015 | Perinuclear theca |
| 37 | 708 | 26.5 | 543 | AA2016 | Human yes1 protei |
| 38 | 701.5 | 26.3 | 1130 | AA2017 | Human Bcr-Abl tyro |
| 39 | 699.5 | 26.2 | 565 | AA2018 | Novel human diagno |
| 40 | 699.5 | 26.2 | 1130 | AA2019 | Human Bcr-Abl tyro |
| 41 | 699.5 | 26.2 | 1130 | AA2020 | Human Bcr-Abl tyro |
| 42 | 698.5 | 26.2 | 1130 | AA2021 | Human Bcr-Abl tyro |
| 43 | 698.5 | 26.2 | 1130 | AA2022 | Human Bcr-Abl tyro |
| 44 | 698.5 | 26.2 | 1130 | AA2023 | Human Bcr-Abl tyro |
| 45 | 697.5 | 26.1 | 1130 | AA2024 | Human Bcr-Abl tyro |

ALIGNMENTS

| RESULT 1 | ID | AA1980 standard; protein: 507 AA. |
|----------|--------|---|
| AA1980 | AA1980 | 25-MAR-2003 (updated) |
| AA1981 | AA1981 | 27-OCT-1995 (first entry) |
| AA1982 | AA1982 | Cytoplasmic tyrosine kinase. |
| AA1983 | AA1983 | Cytoplasmic tyrosine kinase; blood; cell differentiation; |
| AA1984 | AA1984 | screening; anticancer agent; SH3; src homology domain. |
| AA1985 | AA1985 | Human src-c protei |
| AA1986 | AA1986 | Human src-c protei |
| AA1987 | AA1987 | Human src-c protei |
| AA1988 | AA1988 | Human src-c protei |
| AA1989 | AA1989 | Human src-c protei |
| AA1990 | AA1990 | Human src-c protei |
| AA1991 | AA1991 | Human src-c protei |
| AA1992 | AA1992 | Human src-c protei |
| AA1993 | AA1993 | Human src-c protei |
| AA1994 | AA1994 | Human src-c protei |
| AA1995 | AA1995 | Human src-c protei |
| AA1996 | AA1996 | Human src-c protei |
| AA1997 | AA1997 | Human src-c protei |
| AA1998 | AA1998 | Human src-c protei |
| AA1999 | AA1999 | Human src-c protei |
| AA2000 | AA2000 | Human src-c protei |
| AA2001 | AA2001 | Human src-c protei |
| AA2002 | AA2002 | Human src-c protei |
| AA2003 | AA2003 | Human src-c protei |
| AA2004 | AA2004 | Human src-c protei |
| AA2005 | AA2005 | Human src-c protei |
| AA2006 | AA2006 | Human src-c protei |
| AA2007 | AA2007 | Human src-c protei |
| AA2008 | AA2008 | Human src-c protei |
| AA2009 | AA2009 | Human src-c protei |
| AA2010 | AA2010 | Human src-c protei |
| AA2011 | AA2011 | Human src-c protei |
| AA2012 | AA2012 | Human src-c protei |
| AA2013 | AA2013 | Human src-c protei |
| AA2014 | AA2014 | Human src-c protei |
| AA2015 | AA2015 | Human src-c protei |
| AA2016 | AA2016 | Human src-c protei |
| AA2017 | AA2017 | Human src-c protei |
| AA2018 | AA2018 | Human src-c protei |
| AA2019 | AA2019 | Human src-c protei |
| AA2020 | AA2020 | Human src-c protei |
| AA2021 | AA2021 | Human src-c protei |
| AA2022 | AA2022 | Human src-c protei |
| AA2023 | AA2023 | Human src-c protei |
| AA2024 | AA2024 | Human src-c protei |

XX (ASAH) ASAMI KASEI KOGYO KK.
 XX Sakano S;
 PI WPI; 1995-106842/14.
 DR N-PSDB; AAO84888.
 XX
 PT Cytoplasmic tyrosine kinase and antibody recognising it - for
 screening chemical substances for tyrosine kinase inhibitory or
 PT activating activity for use as cancer therapy
 XX
 PS Claim 1; Page 42-44; 58pp; English.
 XX
 CC A cytoplasmic tyrosine kinase which has enhanced expression in
 CC connection with blood cell differentiation has been isolated from the
 CC human U9-7 blood cell line. The DNA sequences and antibodies raised
 CC against the enzyme, are useful for screening agents for inhibiting or
 CC activating activity on the tyrosine kinase, for use as anticancer agents.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 507 AA;
 Query Match 100.0%; Score 2671; DB 16; Length 507;
 Best Local Similarity 100.0%; Pred. No. 8.6e-242;
 Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MAGRGLSVSWRAFHGCDSEAEELPRVSPRFLRAHMPVPSARMPTRMAAGTCITCEHT 60
 1 MAGRGLSVSWRAFHGCDSEAEELPRVSPRFLRAHMPVPSARMPTRMAAGTCITCEHT 60
 61 RPKPGEIARRKGDVVTILEACENKSWYRVKHNHTSGOGLLAAGALREREALSADPKLSLM 120
 61 RPKPGEIARRKGDVVTILEACENKSWYRVKHNHTSGOGLLAAGALREREALSADPKLSLM 120
 121 PMFHGKISGOEAVOQLOPPEDGLFLVRESARHHPGDVYLCSFGRDVIHYRVLHRDGLT 180
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 181 DEAVFPCNLMADWEHNSKDKGALCTKLVPRKRKHGTRKSABEELARAGWMLNLOHLTLGAQ 240
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 241 IGEFEGGAVLQGEYLGOKVAVNKIKCDVTAQAFIDETAAMTKQHNEVLVRLGVIILHOG 300
 241 IGEFEGGAVLQGEYLGOKVAVNKIKCDVTAQAFIDETAAMTKQHNEVLVRLGVIILHOG 300
 301 YIYMEHVSNGNLVNFRTGRALVNTAQLQFSLHVAEGMEYLESKKLVHRDLAARNILY 360
 301 YIYMEHVSNGNLVNFRTGRALVNTAQLQFSLHVAEGMEYLESKKLVHRDLAARNILY 360
 361 SEDLVAKVSDPFGIACKERKGLDSSRLPVKWTAPAEALKHGKFTSKSDVMSFGVILMEVFSY 420
 361 SEDLVAKVSDPFGIACKERKGLDSSRLPVKWTAPAEALKHGKFTSKSDVMSFGVILMEVFSY 420
 421 GRAPYPKMSLKEVSEAVEKGYRMEPEGCGPGVHYVLMSSCWEAEPARRPFRKLAELKAR 480
 421 GRAPYPKMSLKEVSEAVEKGYRMEPEGCGPGVHYVLMSSCWEAEPARRPFRKLAELKAR 480
 481 ELRSAGAPASVSGODADGSTSPRSQEP 507
 481 ELRSAGAPASVSGODADGSTSPRSQEP 507

RESULT 2
 ID AAO15860 standard; Protein; 507 AA.
 AC AAO15860;
 DT 02-JAN-2003 (first entry)
 XX Human matk-related protein.

XX Human; allergic disease; matk gene; atopic dermatitis.
 XX Homo sapiens.
 OS WO200275304-A1.
 PN 26-SEP-2002.
 PD 01-MAR-2002; 2002MO-JP01916.
 PF 21-MAR-2001; 2001JP-0081028.
 PR (GENO-) GENOX RES INC.
 PA (NIGE-) JAPAN GEN AGENCY NATION.
 XX Sugita Y, Heishi M, Kagaya S, Gunji S, Tsujimoto G;
 DR WPI; 2002-750572/81.
 DR N-PSDB; AAL50631.
 XX
 PT Examining allergic diseases by changes in expression level of matk gene
 PT in peripheral monocytes as indication, also applicable in screening
 PT compounds for treating allergic diseases e.g. atopic dermatitis -
 XX Disclosure; Page 52-55; 60pp; Japanese.
 XX
 CC The invention comprises a method of examining allergic diseases, the
 CC method comprises comparing the expression level of the matk gene in a
 CC biological sample of a patient and a healthy individual. The method of
 CC the invention is useful for examining/diagnosing allergic diseases -
 CC particularly atopic dermatitis, the method of the invention is also
 CC useful in screening candidate compounds for remedies. The present amino
 CC acid sequence represents a human matk-related protein.
 XX
 SQ Sequence 507 AA;
 Query Match 100.0%; Score 2671; DB 23; Length 507;
 Best Local Similarity 100.0%; Pred. No. 8.6e-242;
 Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MAGRGLSVSWRAFHGCDSEAEELPRVSPRFLRAHMPVPSARMPTRMAAGTCITCEHT 60
 1 MAGRGLSVSWRAFHGCDSEAEELPRVSPRFLRAHMPVPSARMPTRMAAGTCITCEHT 60
 61 RPKPGEIARRKGDVVTILEACENKSWYRVKHNHTSGOGLLAAGALREREALSADPKLSLM 120
 61 RPKPGEIARRKGDVVTILEACENKSWYRVKHNHTSGOGLLAAGALREREALSADPKLSLM 120
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 121 PMFHGKISGOEAVOQLOPPEDGLFLVRESARHHPGDVYLCSFGRDVIHYRVLHRDGLT 180
 181 DEAVFPCNLMADWEHNSKDKGALCTKLVPRKRKHGTRKSABEELARAGWMLNLOHLTLGAQ 240
 181 DEAVFPCNLMADWEHNSKDKGALCTKLVPRKRKHGTRKSABEELARAGWMLNLOHLTLGAQ 240
 241 IGEFEGGAVLQGEYLGOKVAVNKIKCDVTAQAFIDETAAMTKQHNEVLVRLGVIILHOG 300
 241 IGEFEGGAVLQGEYLGOKVAVNKIKCDVTAQAFIDETAAMTKQHNEVLVRLGVIILHOG 300
 301 YIYMEHVSNGNLVNFRTGRALVNTAQLQFSLHVAEGMEYLESKKLVHRDLAARNILY 360
 301 YIYMEHVSNGNLVNFRTGRALVNTAQLQFSLHVAEGMEYLESKKLVHRDLAARNILY 360
 361 SEDLVAKVSDPFGIACKERKGLDSSRLPVKWTAPAEALKHGKFTSKSDVMSFGVILMEVFSY 420
 361 SEDLVAKVSDPFGIACKERKGLDSSRLPVKWTAPAEALKHGKFTSKSDVMSFGVILMEVFSY 420
 421 GRAPYPKMSLKEVSEAVEKGYRMEPEGCGPGVHYVLMSSCWEAEPARRPFRKLAELKAR 480
 421 GRAPYPKMSLKEVSEAVEKGYRMEPEGCGPGVHYVLMSSCWEAEPARRPFRKLAELKAR 480

QY 481 ELRSAGAPASVSGODADGTSRSPSOEP 507
 |||||||
 Db 481 ELRSAGAPASVSGODADGTSRSPSOEP 507

RESULT 3
 AAR84181
 ID AAR84181 standard; Protein; 507 AA.
 XX AAR84181;

DT 26-MAR-1996 (first entry)

DE Megakaryocyte kinase MKK1.

KM Megakaryocyte kinase-1; MKK1; cytoplasmic tyrosine kinase;
 cellullar signal transduction; leukaemia; thrombocytopenia.

OS Homo sapiens.

Key Location/Qualifiers
 FH Domain 48..111
 FT /label= SH3_domain 122..196
 FT /label= SH2_domain 233..478
 FT Domain /label= Catalytic_domain

PN W09529185-A1.

PD 02-NOV-1995.

PF 24-APR-1995; 95WO-US05008.

PR 21-APR-1995; 95US-0426509.
 PR 22-APR-1994; 94US-0232545.

PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 (SUOE-) SUGEN INC.

PI Gishizky M, Sures I, Ullrich A;

DR WPI; 1995-382959/49.
 DR N-PSDB; AAT00616.

PT New poly:nucleotide(s) encoding megakaryocyte tyrosine kinase(s) -
 PT used to develop prods. for the treatment and diagnosis of kinase
 PT related signal transduction abnormalities.

PS Claim 15; Fig 1A-C; 82pp; English.

CC Human megakaryocyte kinase MKK1 (AAR84181) is a 58 kDa cytosolic
 CC tyrosine kinase showing 54% homology with csk. It appears to play
 CC a regulatory role in the growth and differentiation of
 CC megakaryocytes and perhaps neural tissues. Recombinant MKK1 can be
 CC produced in host cells by expression of encoding cDNA (AAT00616), and
 CC used in the treatment and diagnosis of e.g. leukaemia and
 CC thrombocytopenia.

XX SQ Sequence 507 AA;

Query Match 99.9%; Score 2668; DB 16; Length 507;
 Best Local Similarity 99.8%; Pred. No. 1.6e-241;
 Matches 506; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGRGSLSVSWRAFHGCDSEBELPRVSPRFLRAMHPPVSARMPTRRMAPGTQCITKCEHT 60
 |||||||
 Db 1 MAGRGSLSVSWRAFHGCDSEBELPRVSPRFLRAMHPPVSARMPTRRMAPGTQCITKCEHT 60
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 QY 61 RPKPELAFRRKGDVYTIIEACENKSWYKXKHTSCQEBGLAAGALREDAISADPKLSIM 120
 |||||||
 Db 61 RPKPELAFRRKGDVYTIIEACENKSWYKXKHTSCQEBGLAAGALREDAISADPKLSIM 120
 |||||||

QY 121 PWFHGKISQGEAVOOLQPPEDGLFLVRESARHPGDVILCVSPGRDVIHYRVLRHDCGLTI 180
 |||||||
 Db 121 PWFHGKISQGEAVOOLQPPEDGLFLVRESARHPGDVILCVSPGRDVIHYRVLRHDCGLTI 180
 |||||||
 QY 181 DEAVEFCNMDMVEHYSKDKGAICTKLVPRKRHGTKSAEELARAGMLNTQHLTLGAQ 240
 |||||||
 Db 181 DEAVEFCNMDMVEHYSKDKGAICTKLVPRKRHGTKSAEELARAGMLNTQHLTLGAQ 240
 |||||||
 QY 241 IGEGERGAVLQGEYIGOKVAVNKIKCDVTAQAFLEDTAVMTQHEHNLVRLGLVLIHQGL 300
 |||||||
 Db 241 IGEGERGAVLQGEYIGOKVAVNKIKCDVTAQAFLEDTAVMTQHEHNLVRLGLVLIHQGL 300
 |||||||
 QY 301 YIVMEHVSCKGNLVNFLTFRGRALVMTAQLQPSLVHAEGMEYLESKLVHRDLAARNILV 360
 |||||||
 Db 301 YIVMEHVSCKGNLVNFLTFRGRALVMTAQLQPSLVHAEGMEYLESKLVHRDLAARNILV 360
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 QY 361 SEDLVAKVSDFGIAKAERKGLDSSRLPVKMTAPEALKHGFPSKSDVMSFGVLLMEVESY 420
 |||||||
 Db 361 SEDLVAKVSDFGIAKAERKGLDSSRLPVKMTAPEALKHGFPSKSDVMSFGVLLMEVESY 420
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 QY 421 GRAPYPKMSLKEVSEAVEKGYMEPEEGCGPVHYHLMSSCWEAEPRARRPFRKLAELAR 480
 |||||||
 Db 421 GRAPYPKMSLKEVSEAVEKGYMEPEEGCGPVHYHLMSSCWEAEPRARRPFRKLAELAR 480
 |||||||
 QY 481 ELRSAGAPASVSGODADGTSRSPSOEP 507
 |||||||
 Db 481 ELRSAGAPASVSGODADGTSRSPSOEP 507
 |||||||

RESULT 4
 AAR71132
 ID AAR71132 standard; Protein; 466 AA.

AC AAR71132;

DT 25-MAR-2003 (updated)
 DT 27-OCT-1995 (first entry)

DE N-terminal truncated cytoplasmic tyrosine kinase.

KM cytoplasmic; tyrosine kinase; blood; cell differentiation;
 screening; anticancer agent; SH3; src homology domain.

OS Homo sapiens.

Key Location/Qualifiers
 FH Domain 7..70
 FT /note= "SH3 domain" 81..155
 FT Domain /note= "SH2 domain" 192..438
 FT Domain /note= "tyrosine kinase domain"

PN W09506113-A1.

PD 02-MAR-1995.

PF 25-AUG-1994; 94WO-JP01411.

PR 25-AUG-1993; 93JP-0210403.
 PR 29-MAR-1994; 94JP-0058553.

PA (ASAH) ASAHIT KASEI KOGYO KK.

PI Sakano S;

DR WPI; 1995-106842/14.
 DR N-PSDB; AAO8488.

PT Cytoplasmic tyrosine kinase and antibody recognising it - for
 PT screening chemical substances for tyrosine kinase inhibitory or
 PT activating activity for use as cancer therapy

PS Claim 1; Page 40-42; 58pp; English.

XX A cytoplasmic tyrosine kinase which has enhanced expression in
 CC connection with blood cell differentiation has been isolated from the
 CC human UT-7 blood cell line. This sequence comprises an N-terminal
 CC truncated fragment of the enzyme (residues 42-507 of AAR71133). The DNA
 CC sequences and antibodies raised against the enzyme, are useful for
 CC screening agents for inhibiting or activating activity on the tyrosine
 CC kinase, for use as anticancer agents.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC
 XX Sequence 466 AA:

SO Query Match 91.5%; Score 2444; DB 16; Length 466;
 Best Local Similarity 100.0%; Pred. No. 1.6e-220;
 Matches 466; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 MPTRRRAGPQCCTTCKCHTRPKPGELAFKRGDVYTTILEACENKSWYVKHHTSGOGLLA 101
 DB 1 MPTRRRAGPQCCTTCKCHTRPKPGELAFKRGDVYTTILEACENKSWYVKHHTSGOGLLA 60
 QY 102 AGALRREALSADPKLSLMPFHKISGQEA VOOLPPEDGLFLVRESARHPG DYLCVS 161
 DB 61 AGALRREALSADPKLSLMPFHKISGQEA VOOLPPEDGLFLVRESARHPG DYLCVS 120
 QY 162 FGRDVIHYRYLHRDGHLLTIDEAVFPCNLMDVHEHYSKDKGALCTKLVPRKRKHTGSAEE 221
 DB 121 FGRDVIHYRYLHRDGHLLTIDEAVFPCNLMDVHEHYSKDKGALCTKLVPRKRKHTGSAEE 180
 QY 222 ELARAGMLNLQHLTTGAQIGEGEFGAVLOGEYLGVKAVANKIKCDVTAQAFIDETAVMT 281
 DB 181 ELARAGMLNLQHLTTGAQIGEGEFGAVLOGEYLGVKAVANKIKCDVTAQAFIDETAVMT 240
 QY 282 KMCHENLVRLGLYLHOGILTYVMEHYSKGNLVNLFRTGRALVNTAQLQFSLHVAEGME 341
 DB 241 KMCHENLVRLGLYLHOGILTYVMEHYSKGNLVNLFRTGRALVNTAQLQFSLHVAEGME 300
 QY 342 YLESKLVHRDLAARNILVSEDLVAVKVSDFGLAKAERKGLDSSRLPYKWTAPALKHGRF 401
 DB 301 YLESKLVHRDLAARNILVSEDLVAVKVSDFGLAKAERKGLDSSRLPYKWTAPALKHGRF 360
 QY 402 TSKSDVWSPFGLVLMVEFVSGRAPYPKMSLKEVSEAVKGRMPBEGCPGVHVMSSCW 461
 DB 361 TSKSDVWSPFGLVLMVEFVSGRAPYPKMSLKEVSEAVKGRMPBEGCPGVHVMSSCW 420
 QY 462 EAPRRRPPPRKLAELKRLSAGAPASVSGODADGSTSPRSQEP 507
 DB 421 EAPRRRPPPRKLAELKRLSAGAPASVSGODADGSTSPRSQEP 466

RESULT 5
 AAM64454
 ID AAM64454 standard; Protein; 528 AA.
 XX
 AC AAM64454;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Human matk protein.
 XX
 KW Breast; cancer; matk; CSK homologous kinase; CHK; detection; diagnosis;
 KW cytoplasmic protein; tyrosine kinase; ErbB-2; negative regulator;
 KW mitogenic signalling.
 XX
 OS Homo sapiens.
 XX
 PN MO9830704-A1.
 XX
 PD 16-JUL-1998.
 XX
 PF 07-JAN-1998; 98MO-US00420.
 XX
 PR 16-JUN-1997; 97US-0876882.

PR 08-JAN-1997; 97US-0035228.
 XX
 PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
 XX
 PI Avraham H, Groopman JE;
 XX
 DR WPI; 1998-399149/34.
 DR N-PSDB; AAV44497.
 XX
 PT Detecting breast cancer by detecting Csk homologous kinase
 PT expression - especially in humans and use of Csk homologous kinase
 PT in treatment or prophylaxis of breast cancer and for producing
 PT medicaments
 PS
 XX Disclosure; Fig 2; 54pp; English.

CC This sequence represents a CSK homologous kinase (CHK) which is used in a
 CC method of detecting cancer in breast tissue. The method allows diagnosis
 CC of breast cancer in mammals, especially humans. It is based on the
 CC discovery that a cytoplasmic protein tyrosine kinase, CHK, is expressed
 CC in human breast tissue, but not in adjacent tissue. This protein can be
 CC used to raise antibodies which can be included in compositions and
 CC diagnostic kits for diagnosis of breast cancer. The presence of CHK in
 CC breast tissue can also be determined using other standard methods (e.g.
 CC Northern blotting) or by detecting nucleic acid sequences encoding all/a
 CC portion of the protein (e.g. using hybridisation probes). Over-expression
 CC of the receptor tyrosine kinase ErbB-2 has previously been associated
 CC with the development of breast cancer, and CHK specifically interacts
 CC with activated ErbB-2, and may function as a negative regulator of
 CC ErbB-2 mediated mitogenic signalling. The compositions may also be used
 CC to design drugs (e.g. which incorporate CHK analogues with greater
 CC biological activity than CHK) and to identify CHK antagonists and
 CC agonists for therapeutic use.
 CC
 XX Sequence 528 AA:

SO Query Match 91.1%; Score 2434.5; DB 19; Length 528;
 Best Local Similarity 93.3%; Pred. No. 1.5e-219;
 Matches 472; Conservative 1; Mismatches 18; Indels 15; Gaps 3;

QY 1 MAGRGLSVSRFAFGDSAEFLPRVSPRFLRAHPPVSAKMTPTRRAPGTCITCEHT 60
 DB 1 MAGRGLSVSRFAFGDSAEFLPRVSPRFLRAHPPVSAKMTPTRRAPGTCITCEHT 60
 QY 61 RPKPGEIAFRKGGVNTI-LEACENKSWYRKHNTSGOGLLAAGALRREALSADPKLSL 119
 DB 61 RPKPGEIAFRKGGVNTI-LEACENKSWYRKHNTSGOGLLAAGALRREALSADPKLSL 120
 QY 120 MPWFHKGISGQEA VOOLPPEDGLFLVRESARHPG DYLCVSFGRDVIHYRYLHRDGHLLT 179
 DB 121 MPWFHKGISGQEA VOOLPPEDGLFLVRESARHPG DYLCVSFGRDVIHYRYLHRDGHLLT 180
 QY 180 IDEAVFPCNLMDVHEHYSKDKGALCTKLVPRKRKHTGKSAEELARAGMLNLQHLTTGA 239
 DB 181 IDEAVFPCNLMDVHEHYSKDKGALCTKLVPRKRKHTGKSAEELARAGMLNLQHLTTGA 240
 QY 240 QIGEGEFGAVLOGEYLGVKAVANKIKCDVTAQAFIDETAVMTKMCHENLVRLGLYLHOG 299
 DB 241 QIGEGEFGAVLOGEYLGVKAVANKIKCDVTAQAFIDETAVMTKMCHENLVRLGLYLHOG 300
 QY 300 LTYVMEHYSKGNLVNLFRTGRALVNTAQLQFSLHVAEGMEYLESKLVHRDLAARNIL 359
 DB 301 LTYVMEHYSKGNLVNLFRTGRALVNTAQLQFSLHVAEGMEYLESKLVHRDLAARNIL 360
 QY 360 VSEDVAVKVSDFGLAERKGLDSSRLPYKWTAPALKHGRFSTKSDVWSPFGLVMEVS 419
 DB 361 VSEDVAVKVSDFGLAERKGLDSSRLPYKWTAPALKHGRFSTKSDVWSPFGLVMEVS 419
 QY 420 YGRAPYPKMSLKEVSEAVKGRMPBEGCPGVHVMSSCWAEAPRRRPPPRKLAELK 479
 DB 420 YGRAPYPKMSLKEVSEAVKGRMPBEGCPGVHVMSSCWAEAPRRRPPPRKLAELK 479
 QY 480 RELRSAGAPASVSGODADGSTSPRSQ 505

Db 471 ----SANNPRSMPSYAVQVPPSPQ 492

RESULT 6
AAU99575
ID AAU99575 standard; Protein; 415 AA.
XX
AC AAU99575;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human kinase related to tyrosine kinase family.
XX
KW Human; kinase; tyrosine kinase; kinase mediated disorder;
KW haematopoietic disorder; cell signal transduction disorder;
KW cancer; haemostatic; cyostatic; enzyme.
XX
OS Homo sapiens.
XX
PN WO200252018-A2.
XX
PD 04-JUL-2002.
XX
PF 19-DEC-2001; 2001WO-US48546.
XX
PR 21-DEC-2000; 2000US-0741154.
XX
PA (PEKE) PE CORP NY.
XX
PI Beasley EM, Shao W, Ketchum K, Di Francesco V;
XX
DR WPI: 2002-583568/62.
XX
DR N-PSDB; ABR88791, ABR88792.
XX
PT New isolated human kinase proteins and genes, useful in developing
PT drugs, as well as for diagnosing, preventing or treating disorders
PT associated with defective cell signal transduction, e.g. cancer or
PT haematopoietic disorders .
XX
PS Claim 1; Fig 2A; 78pp; English.
XX
CC The present invention relates to the isolation of a novel human kinase
CC related to the tyrosine kinase family, and polynucleotide sequences
CC encoding it. The gene encoding the kinase of the invention maps to
CC chromosome 19. The kinase may be used for identifying a modulator of
CC the kinase, an agent that binds to the kinase, or for identifying
CC other members of the family. The kinase may also be used to raise
CC antibodies which may be used in immunoassays or drug screening assays.
CC The sequences of the invention may be used for treating a disease or
CC condition mediated by a human kinase such as haematopoietic disorders
CC and other disorders associated with defective cell signal transduction
CC (e.g. cancer). The polynucleotide sequences encoding the kinase are
CC useful for isolating and purifying the kinase, and as probes or primers.
CC The present sequence represents the human kinase of the invention.
XX
SQ Sequence 415 AA:
XX
Query Match 75.3%; Score 2012; DB 23; Length 415;
Best Local Similarity 100.0%; Pred. No. 5e-180;
Matches 386; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

122 WFHGKISGOEAVQQLQPPEDGFLTVRESARHPGVDYLCVSEGRDVIHYRVLHRDGLTLD 181
|||||
30 WFHGKISGOEAVQQLQPPEDGFLTVRESARHPGVDYLCVSEGRDVIHYRVLHRDGLTLD 89
|||||

182 EAVFECNLMDEWEHRSKGAICTLVPRKRGHGRKSAEELARAGMLNLOHTLGAOI 241
|||||
90 EAVFECNLMDEWEHRSKGAICTLVPRKRGHGRKSAEELARAGMLNLOHTLGAOI 149
|||||

242 GEGGGAVALGEGYLGOKYAVVKNKCDVTAQAFLDETAVMFTKQHNELVRLGLVILHOGGLY 301
|||||
150 GEGGGAVALGEGYLGOKYAVVKNKCDVTAQAFLDETAVMFTKQHNELVRLGLVILHOGGLY 209
|||||

QY 302 IYMEHVSQGNLVNFIPTNGRALVNTAQLLOSLHVAEGMEYIESKKLYHRDLAARNILVS 361
|||||
Db 210 IYMEHVSQGNLVNFIPTNGRALVNTAQLLOSLHVAEGMEYIESKKLYHRDLAARNILVS 269
|||||

QY 362 EDLVAKVSDPGLAKERRKGLDSSRLPVKMTPEALKHGRKFSKSDVMSFGVLLMEVFSYG 421
|||||
Db 270 EDLVAKVSDPGLAKERRKGLDSSRLPVKMTPEALKHGRKFSKSDVMSFGVLLMEVFSYG 329
|||||

QY 422 RAPPYKMSLKEVSEAVEKGYRMEPEGCGPVPVHVLMSQWAEAPARRPPFRKLAEKLARE 481
|||||
Db 330 RAPPYKMSLKEVSEAVEKGYRMEPEGCGPVPVHVLMSQWAEAPARRPPFRKLAEKLARE 389
|||||

QY 482 LRSAGAPASVSGQDADGSTSPRSQDP 507
|||||
Db 390 LRSAGAPASVSGQDADGSTSPRSQDP 415
|||||

RESULT 7
AAR71131
ID AAR71131 standard; Protein; 246 AA.
XX
AC AAR71131;
XX
XX
DT 25-MAR-2003 (updated)
DT 27-OCT-1995 (first entry)
XX
DE Tyrosine kinase domain of cytoplasmic tyrosine kinase.
XX
XX
KW cytoplasmic; tyrosine kinase; blood; cell differentiation;
KW screening; anticancer agent.
XX
OS Homo sapiens.
XX
PN WO9506113-A1.
XX
PD 02-MAR-1995.
XX
PF 25-AUG-1994; 94WO-JP01411.
XX
PR 25-AUG-1993; 93JP-0210403.
PR 29-MAR-1994; 94JP-0058553.
XX
PA (ASAH) ASAH1 KASEI KOGYO KK.
XX
PI Sakano S;
XX
DR WPI: 1995-106842/14.
DR N-PSDB; AAO84888.
XX
PT Cytoplasmic tyrosine kinase and antibody recognising it - for
PT screening chemical substances for tyrosine kinase inhibitory or
PT activating activity for use as cancer therapy
XX
PS Claim 1; Page 39; 58pp; English.
XX
CC A cytoplasmic tyrosine kinase which has enhanced expression in
CC connection with blood cell differentiation has been isolated from the
CC human UT-7 blood cell line. This sequence comprises the tyrosine
CC kinase domain of the enzyme (residues 197-437of AAR71132; residues
CC 233-478 of AAR71133). The DNA sequences and antibodies raised against
CC the enzyme, are useful for screening agents for inhibiting or activating
CC activity on the tyrosine kinase, for use as anticancer agents.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 246 AA:
XX
Query Match 47.2%; Score 1261; DB 16; Length 246;
Best Local Similarity 99.6%; Pred. No. 7.9e-110;
Matches 245; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

233 OHLTGAQIGGEGFAVLGEGYLGOKYAVVKNKCDVTAQAFLDETAVMFTKQHNELVRL 292
|||||

Db 1 QHLLTGAQIGEGFAGVLAQGEYIGQKVAANKIKCDVTAQAFLEDTAVTMKQHENLVLL 60
QY 293 GVILHOGGLTYIMEVHSKGNLVNPLRTGRALVNTAQLLOPFLSHVAEGMEYLESKLYHRD 352
Db 61 GVILHOGGLTYIMEVHSKGNLVNPLRTGRALVNTAQLLOPFLSHVAEGMEYLESKLYHRD 120
QY 353 LAARNILVSEDLVAKVSDPGLAKAERKGLDSSRLPVKWTAPALAKHGKFTSKSDVMSFGV 412
Db 121 LAARNILVSEDLVAKVSDPGLAKAERKGLDSSRLPVKWTAPALAKHGKFTSKSDVMSFGV 180
QY 413 LLMVEFSYGRAPYKMSLKEVSEAVEKGRPEPGCPGVHVLMSCEMEAPRRPFR 472
Db 181 LLMVEFSYGRAPYKMSLKEVSEAVEKGRPEPGCPGVHVLMSCEMEAPRRPFR 240
QY 473 KIAEKL 478
Db 241 KIAEKL 246
RESULT 8
AA013873 ID AA013873 standard; Protein; 459 AA.
XX AC AA013873;
XX DT 06-NOV-2001 (first entry)
XX DE Human polypeptide SEQ ID NO 27765.
XX XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; hematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX OS Homo sapiens.
XX PN WO200164835-A2.
XX PD 07-SEP-2001.
XX PF 26-FEB-2001; 2001WO-US04927.
XX PR 28-FEB-2000; 2000US-0515126.
XX PR 18-MAY-2000; 2000US-0577409.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Drmanac RT;
XX DR WPI; 2001-514838/56.
XX DR N-PSDB; AA193804.
XX PT Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders -
PS Claim 20: SEQ ID NO 27765; 1399pp + Sequence Listing; English.
XX XX The invention relates to human polynucleotides (AA179941-AA193841) and
CC the encoded proteins (AA000010-AA013910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

SO Sequence 459 AA;
Query Match 46.7%; Score 1247.5; DB 22; Length 459;
Best Local Similarity 53.2%; Pred. No. 3.7e-108;
Matches 238; Conservative 82; Mismatches 118; Indels 9; Gaps 3;
QY 40 ARMPTR-----RWAPGTQCITKCEHTPRPGELAFKRGDVVITLEACENKSWRYVKNHT 93
Db 4 ARAPKMSAIAQAMPSCSTECIAKYNFNGTAQEDLPFCRGDVLTIVATKDPNNYKAKNKV 63
QY 94 SGQEGLLAALALREKRLASDPKLSLMPWHGKISQGEAVQQLQPPEDGFLYRESRHP 153
Db 64 -GREGIIPANYVOKREGVKAGTKLSLMPWHGKITRQARLLYPPETGLFLVRESTNYP 122
QY 154 GDVYLVSFGRDVIHYHVLNRDGLLTIDEAVFPCNLMDVYEHYSKDGAICTKLVPRRK 213
Db 123 GDYTLVCSCDCKVEHRYIMHASKLSIDEVYENLMQVJHNTSDADGCTLIRPKM 182
QY 214 HGTKSAEELARAGWLINLQHLTGAQIGEGFAGVLAQGEYIGQKVAANKIKCDVTAQAF 273
Db 183 EGTVAQADEFFYRSGMALNMKELKLTQIGKGEFGDVMLGDRGNKVAVKCIKMDATAQAF 242
QY 274 LDETAVTMKQHENLVRLGLVILHQ--GLTYIMEVHSKGNLVNPLRTGRALVNTAQLLO 331
Db 243 LAEASVNTQLRHSNLVQLGLVIEBKGLTYIYEMAKGSLVDTLNSRGSVLGGDCLK 302
QY 332 FSLHVAEGMEYLESKLYHRDLAARNILVSEDLVAKVSDPGLAKAERKGLDSSRLPVKWT 391
Db 303 FSLDVCAMLEYLSEGNNVVHRDLAARNILVSEDLVAKVSDPGLAKAERKGLDSSRLPVKWT 362
QY 392 APEALKHGKFTSKSDVMSFGVLLMEVFSYGRAPYKMSLKEVSEAVEKGRPEPGCPG 451
Db 363 APEALREKFKSTSDVMSFGVLLMEVFSYGRAPYKMSLKEVSEAVEKGRPEPGCPG 422
QY 452 PVTLMSSCEMEAPRRPFRKIAEKL 478
Db 423 AYTEVMKNCWHLDAAMPSTQLREQL 449
RESULT 9
AAV44448 ID AAV44448 standard; Protein; 450 AA.
XX AC AAV44448;
XX DT 22-MAR-2000 (first entry)
XX DE Wild-type human c-Src tyrosine kinase.
XX KW Angiogenesis; tyrosine kinase; Src; inhibition; activation; modulate;
KW human; viral expression vector; replication competent; mutant Src;
KW inflammatory disease; arthritis; rheumatoid arthritis; restenosis;
KW diabetic retinopathy; osteoporosis; cancer.
XX OS Homo sapiens.
XX PN WO9961590-A1.
XX PD 02-DEC-1999.
XX PF 28-MAY-1999; 99WO-US11780.
XX PR 29-MAY-1998; 98US-0087220.
XX PA (SCRI) SCRIPPS RES INST.
XX PI Cheresah DA, Eliceiri B, Schwartzberg PL;
XX DR WPI; 2000-116335/10.
XX DR N-PSDB; AA229701.
XX PT Using tyrosine kinase Src for modulating angiogenesis in tissues useful
PT in, e.g. treatment of chronic articular rheumatism -


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RESULT 11
AAB84662
ID AAB84662 standard; Protein; 450 AA.
XX
AC AAB84662:
XX
DT 05-SEP-2001 (first entry)
XX
DE Amino acid sequence of human tyrosine kinase protein Src.
XX
KM Vascular permeability; tyrosine kinase protein; Src; Yes; stroke;
KM myocardial infarction; restenosis; trauma; blood vessel; atherosclerosis;
KM diabetic retinopathy; inflammatory disease; infection; arthritis;
KM adult respiratory distress syndrome; ARDS; rheumatoid arthritis;
KM diabetic retinopathy; psoriasis; neovascular glaucoma;
KM capillary proliferation; osteoporosis; cancer.
XX
OS Homo sapiens.
XX
PN WO200145751-A1.
XX
PD 28-JUN-2001.
XX
PF 22-DEC-2000; 2000WO-US35396.
XX
PR 22-DEC-1999; 99US-0470881.
PR 29-MAR-2000; 2000US-0538248.
XX
PA (SCRI ) SCRIpps RES INST.
XX
PI Cheresah DA, Eljcelri B, Paul R;
XX
DR N-PSDB; AAH28358.
XX
PT WPI: 2001-417982/44.
XX
PT Modulating vascular permeability in tissues, including inflamed tissue,
PT tissues associated with stroke, myocardial infarction, by contacting
PT the tissue with tyrosine kinase protein Src, Yes or their modified
PT forms.
XX
PS Disclosure; Fig 4; 133pp; English.
XX
CC The specification describes a method for modulating vascular
CC permeability in a tissue suffering from a disease condition. The method
CC comprises contacting the tissue with a pharmaceutical composition
CC comprising tyrosine kinase protein Src, Yes or their mixtures or
CC nucleic acid expressing them. The method is useful for modulating
CC vascular permeability in tissues, including inflamed tissue, tissues
CC associated with stroke, myocardial infarction or other blockage of
CC normal flow, tissues undergoing restenosis, psoriatic, retinal tissue
CC and similar tissues. Pathologies which may be treated include
CC trauma to blood vessels, and other systemic pathological events such as
CC atherosclerosis, diabetic retinopathy, inflammatory disease due to
CC infection by microbial agents and arthritis. Other diseases which can
CC be treated include adult respiratory distress syndrome (ARDS), rheumatoid
CC arthritis, diabetic retinopathy, psoriasis, neovascular glaucoma,
CC capillary proliferation in atherosclerotic plaques and osteoporosis and.
CC cancer associated disorders such as solid tumours, solid tumour
CC metastases, angiofibromas and hemangiomas. The present sequence
CC represents human Src, and is used in the method of the invention.
XX
SQ Sequence 450 AA:
Query Match 46.6%; Score 1245.5; DB 22; Length 450;
Best Local Similarity 54.1%; Pred. No. 5.5e-108;
Matches 225; Conservative 81; Mismatches 115; Indels 3; Gaps 2;
OY 47 MARGTCTRCCEHTFRKPELAEFRKGDVYITLAECKNSWYRVKHTTSQEGHLAGALR 106
DB 8 WPGGTGCIKAYNPHGTAEDDLPKCGDVLIVAVTDPMMYKAKNV-GREGIIPANYO 66
OY 107 ERRAALSDRLSLMPFHGKISQGEAVQOLQPPEDDLFLVRSARHPGDVILCVSGRD 166

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DB 67 KREGVAKGTIKLSLMPFHGKIRTEQAERLLYPETGLFLVRESTNPGDYTLVCSCDGK 126
OY 167 IHRVRLHRDGHILIDEAVFPCNLMDVVEHYSKDGAICIKLVKPKRKHGTSAEELARA 226
DB 127 EHRIRVYHASKLSIDEVYFENLMQVLEHTSDADGICLTRLKPKVMEGTVAADDFYS 186
OY 227 GWLLNLQHLTLGAQIGEGGAVLOGEYLQGVAAVKNIKCDVTAQAFIDETAVMTRMOHE 286
DB 187 GWALNMKEIKLLOTIGKGEFGDVMIGDYGNKRVAVACIKNDATQAFLAEASVMQOLRS 246
OY 287 NIVRLIGVTLHQ--GIYIMEHVSKGNLVNFLTGRALVNTAQLLOFSLHAEGMEYLE 344
DB 247 NVQOLLGVIEERKGLYITEYMAKSLVDYLRSGRSVLGDCCLKESLDVCEAMEYLE 306
OY 345 SKLVYRDAAARNILVSEDLVAVKSPDGLAKAERKGLDSSRLPVKWTAPALHKGFTSK 404
DB 307 GNNFVHRLAARNVLVSEDNVAKVSPDGLTKEASSPDGKLPVKTAPALREKFFSK 366
OY 405 SDVWSFVLLMEVFSYGRAPYPRKMSLKEVSEAVEKGRMEPPGCGPVHVLMSCEAE 464
DB 367 SDVWSFGILLMEYFSGRVPRIPDKDVVPRVEKGYKMDADPGCPAVYEVKMKWHLD 426
OY 465 PARPPPEKLAELK 478
DB 427 AAMRPSFIQLRQOL 440
RESULT 12
AAG67444
ID AAG67444 standard; Protein; 450 AA.
XX
AC AAG67444;
XX
DT 26-NOV-2001 (first entry)
XX
DE Amino acid sequence of a human polypeptide.
XX
KM Human; protein kinase; protein phosphatase; signal transduction;
KM intracellular signalling pathway.
XX
OS Homo sapiens.
XX
PN WO200109345-A1.
XX
PD 08-FEB-2001.
XX
PF 28-JUL-2000; 2000WO-JP05060.
XX
PR 29-JUL-1999; 99JP-0248036.
PR 18-OCT-1999; 99US-0159590.
PR 11-JAN-2000; 2000JP-0118776.
PR 17-FEB-2000; 2000US-0183322.
PR 02-MAY-2000; 2000JP-0183767.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;
PI Senoo C, Nezu J;
XX
DR WPI: 2001-564736/63.
XX
PT New genes encoding protein kinase and protein phosphatase, useful for
PT identifying modulators which can be used to treat human or animal
PT disorders associated with the expression or function of these enzymes -
PS Example 4; Page 249-252; 336pp; Japanese.
XX
CC The specification describes human protein kinase/protein phosphatases.
CC The polypeptides are expected to participate in signal transduction
CC in cells. The kinase phosphatases are connected with intracellular
CC signalling pathways. Antisense oligonucleotides and compounds
CC identified by screening (agonists or antagonists) can be used to

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Db      467 FPGDYTLVCVCFQSKVEHYRVAYLLENKLTIDEEFFENLQGLVAHYEADADGLCTQLIKCL 526
QY      212 RKHGTRK---AEEELARAGWILNQHILTLGAQIGEEFEGANLQGEYLGOKVAVKNIKCDV 268
Db      527 PKLGKQFCJNSKDFVDKGVIPAEALQLRRESIGKGEFGDMLGILRNEKVAVMKLKDEG 586
QY      269 TQAFLDETVAMTMQEHENLVRLLGVIL-HQGLYIVMEHVSNGNLVNFLLPTRGALVNTA 327
Db      587 AVQKFLAEASVMTLLEHNDLVKFIGLVFTSKHLVLYTEYMSKGLVDYLRSGRQHITTK 646
QY      328 QLOFSLHVAEGMEYLESKKLVHRDLARNILVSEDLVAKVSDGLAKAERRGLDSSRLP 387
Db      647 DOIIFAYDTASGMEELEAKKVHRDLAARNVLISEDCAKVSDEGLAREECYNLDVGKLP 706
QY      388 VKMTAPALKHGKFTSKSDVMSFGVLLMEVFSYGRAPYPKMSTLKEVSEAVEKGYRMEPE 447
Db      707 IKMTAPALKNGRFSNKSMDMSFGILMEIYSFGVRPPIPLADVYKHHVEVGTKMEAPE 766
QY      448 GCPGPHVHLMSSCWEAEPPARRPPPKLAEKL 478
Db      767 GCPEIYEMMRQAMDNLNPAKRPFAELKVKL 797

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Search completed: July 29, 2003, 09:50:57
 Job time : 47 secs

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OM protein - protein search, using sw model

Run on: July 29, 2003, 09:47:52 ; Search time 16 Seconds

(without alignments)
1490.155 Million cell updates/sec

Title: US-09-977-261-2

Perfect score: 2671
Sequence: 1 MAGRSLVSWRAHFGDSAE.....PASVSGDDADGSTRSPSQEP 507

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | ID | Description |
|------------|--------|--------------------|--------|-------------|
| 1 | 2671 | 100.0 | 507 1 | MATK_HUMAN |
| 2 | 2332 | 87.3 | 505 1 | MATK_MOUSE |
| 3 | 2221.5 | 83.2 | 467 1 | MATK_RAT |
| 4 | 1253.5 | 46.9 | 450 1 | CSK_CHICK |
| 5 | 1245.5 | 46.6 | 450 1 | CSK_HUMAN |
| 6 | 1242.5 | 46.5 | 450 1 | CSK_RAT |
| 7 | 1227.5 | 46.0 | 450 1 | CSK_MOUSE |
| 8 | 762.5 | 28.5 | 507 1 | LCK_CHICK |
| 9 | 744.5 | 27.9 | 508 1 | LCK_MOUSE |
| 10 | 742.5 | 27.8 | 508 1 | LCK_HUMAN |
| 11 | 735.5 | 27.5 | 526 1 | SRC_RSVR |
| 12 | 734.5 | 27.5 | 568 1 | SRC_AVISR |
| 13 | 734 | 27.5 | 557 1 | SRC_AVISR |
| 14 | 733 | 27.4 | 532 1 | SRC_CHICK |
| 15 | 731.5 | 27.4 | 526 1 | SRC_AVISR |
| 16 | 731.5 | 27.4 | 587 1 | SRC_AVISR |
| 17 | 727.5 | 27.2 | 523 1 | SRC_RSVP |
| 18 | 727 | 27.2 | 535 1 | SRC_HUMAN |
| 19 | 726 | 27.2 | 531 1 | SRC1_XENLA |
| 20 | 724.5 | 27.1 | 526 1 | HCK_HUMAN |
| 21 | 724.5 | 27.1 | 526 1 | SRC_RSVP |
| 22 | 724 | 27.1 | 531 1 | SRC2_XENLA |
| 23 | 724 | 27.1 | 1520 1 | ABL_DROME |
| 24 | 723.5 | 27.1 | 526 1 | SRC_RSVP |
| 25 | 716.5 | 26.8 | 535 1 | SRC_RAT |
| 26 | 716 | 26.8 | 505 1 | SRC1_XENLA |
| 27 | 714 | 26.7 | 540 1 | SRC_MOUSE |
| 28 | 713 | 26.7 | 506 1 | SRK4_XENLA |
| 29 | 713 | 26.7 | 511 1 | LXN_RAT |
| 30 | 710 | 26.6 | 541 1 | YES_MOUSE |
| 31 | 710 | 26.6 | 543 1 | YES_HUMAN |
| 32 | 709 | 26.5 | 536 1 | FYN_XIPHE |
| 33 | 707 | 26.5 | 504 1 | HCK_MACPA |

| | | | | | |
|----|-------|------|-------|-----------|---------------------|
| 34 | 707 | 26.5 | 511 1 | LXN_HUMAN | P07948 homo sapien |
| 35 | 706.5 | 26.5 | 524 1 | HCK_MOUSE | P08103 mus musculus |
| 36 | 706 | 26.4 | 511 1 | LXN_MOUSE | P25911 mus musculus |
| 37 | 706 | 26.4 | 541 1 | YES_CHICK | P09324 gallus galli |
| 38 | 705 | 26.4 | 544 1 | YES_XIPHE | P27447 xiphophorus |
| 39 | 700.5 | 26.2 | 503 1 | HCK_RAT | P50543 ratius norv |
| 40 | 700 | 26.2 | 537 1 | YES_XENLA | P10936 xenopus lae |
| 41 | 699.5 | 26.2 | 535 1 | YRK_CHICK | P02977 gallus galli |
| 42 | 699 | 26.2 | 498 1 | BLK_MOUSE | P16277 mus musculus |
| 43 | 699 | 26.2 | 822 1 | PER_HUMAN | P16591 homo sapien |
| 44 | 698.5 | 26.2 | 536 1 | FYN_HUMAN | P06241 homo sapien |
| 45 | 698.5 | 26.2 | 536 1 | FYN_XENLA | P13406 xenopus lae |

ALIGNMENTS

| RESULT 1 | ID | MATK_HUMAN | STANDARD | PRT | 507 AA. |
|----------|--|------------|----------|-----|---------|
| AC | P42679; | | | | |
| DT | 01-NOV-1995 (Rel. 32, Created) | | | | |
| DT | 01-NOV-1995 (Rel. 32, Last sequence update) | | | | |
| DT | 15-SEP-2003 (Rel. 42, Last annotation update) | | | | |
| DE | Megakaryocyte-associated tyrosine-protein kinase (EC 2.7.1.112) | | | | |
| DE | (tyrosine-protein kinase CTK) (protein kinase HYL) (hematopoietic | | | | |
| DE | consensus tyrosine-lacking kinase). | | | | |
| GN | MATK OR CTK OR HYL. | | | | |
| OS | Homo sapiens (Human). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. | | | | |
| OX | NCBI_TaxID=9606; | | | | |
| RN | [1] | | | | |
| RX | SEQUENCE FROM N.A. | | | | |
| RA | MEDLINE=94181267; PubMed=8134117; | | | | |
| RA | Sakano S., Iwama A., Inazawa J., Ariyama T., Ohno M., Suda T.; | | | | |
| RT | "Molecular cloning of a novel non-receptor tyrosine kinase, HYL | | | | |
| RT | (hematopoietic consensus tyrosine-lacking kinase)."; | | | | |
| RL | Oncogene 9:1155-1161(1994). | | | | |
| RN | [2] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | TISSUE=Megakaryocytes; | | | | |
| RX | MEDLINE=94117408; PubMed=8288563; | | | | |
| RA | Bennett B.D., Cowley S., Jiang S., London R., Deng B., Grabarek J., | | | | |
| RA | Groopman J.E., Goeddel D.V., Avraham H.; | | | | |
| RT | "Identification and characterization of a novel tyrosine kinase from | | | | |
| RT | megakaryocytes."; | | | | |
| RL | J. Biol. Chem. 269:1068-1074(1994). | | | | |
| RN | [3] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RX | MEDLINE=95130565; PubMed=7530249; | | | | |
| RA | Avraham S., Jiang S., Ota S., Fu Y., Deng B., Dowler L.L., | | | | |
| RA | White R.A., Avraham H.; | | | | |
| RT | "Structural and functional studies of the intracellular tyrosine | | | | |
| RT | kinase MATK gene and its translated product."; | | | | |
| RL | J. Biol. Chem. 270:1833-1842(1995). | | | | |
| RN | [4] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RP | Lamerdin J.E., McGready P.M., Skowronski E., Viswanathan V., | | | | |
| RA | Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S., | | | | |
| RA | Puhn H., Velasco N., De L., Regala W., Terry A., Ganes J., | | | | |
| RA | Dargahan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S., | | | | |
| RA | Attix C., Andreise T., Trankheim M., Amico-Keller G., Coefield J., | | | | |
| RA | Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B., | | | | |
| RA | Atefano A., Saunders C., Ow D., Nolan M., Trong S., Kobayashi A., | | | | |
| RL | Olsen A.S., Carrara A.V.; | | | | |
| RL | Submitted (Oct-1998) to the EMBL/GenBank/DBJ databases. | | | | |
| RN | [5] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | TISSUE=Eye; | | | | |
| RX | MEDLINE=22388257; PubMed=12477932; | | | | |
| RA | Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., | | | | |
| RA | Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., | | | | |

| | | | |
|----|-----|-----------------------------|-----|
| QY | 481 | ELRSAGAPASVSGQDADGSTSPRSQEP | 507 |
| | | | |
| Db | 481 | ELRSAGAPASVSGQDADGSTSPRSQEP | 507 |

| RESULT 2 | MATK_MOUSE | STANDARD: | PRT: | 505 AA. |
|----------|--|-----------|------|---------|
| ID | MATK_MOUSE | | | |
| AC | P41242; | | | |
| DT | 01-FEB-1995 (Rel. 31, Created) | | | |
| DT | 01-FEB-1996 (Rel. 33, Last sequence update) | | | |
| DT | 15-SEP-2003 (Rel. 42, Last annotation update) | | | |
| DE | Megakaryocyte-associated tyrosine-protein kinase (EC 2.7.1.112) | | | |
| DE | (tyrosine-protein kinase CTK) (protein kinase NTK). | | | |
| CN | MATK OR CTK OR NTK. | | | |
| OS | mus musculus (Mouse). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | |
| OX | NCBI_Taxid=10090; | | | |
| RN | [1] | | | |
| RP | SEQUENCE OF 41-505 FROM N.A. | | | |
| RC | TISSUE=Brain; | | | |
| RX | MEDLINE=94195789; PubMed=7511815; | | | |
| RA | Klauges S., Adam D., Class K., Fargnoli J., Bolen J.B., | | | |
| RT | Penhallow R.C.; | | | |
| RT | "Ctk: a protein-tyrosine kinase related to Csk that defines an enzyme | | | |
| RT | family."; | | | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 91:2597-2601(1994). | | | |
| RN | [2] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | STRAIN=BALB/C; TISSUE=Thymus; | | | |
| RX | MEDLINE=94255451; PubMed=8197166; | | | |
| RA | Chow L.M.L., Jarvis C.D., Hu Q., Nye S.H., Gervais F.G., | | | |
| RT | Velllette A., Mattis L.A.; | | | |
| RT | "Nk: a Csk-related protein-tyrosine kinase expressed in brain and T | | | |
| RT | lymphocytes."; | | | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 91:4975-4979(1994). | | | |
| RN | [3] | | | |
| RP | SEQUENCE OF 41-505 FROM N.A. | | | |
| RC | STRAIN=DDY/STD; | | | |
| RX | MEDLINE=95206787; PubMed=7899836; | | | |
| RA | Kaneko Y., Nonoguchi K., Fukuyama H., Takano S., Higashitsuji H., | | | |
| RT | Nishiyama H., Takenawa J., Nakayama H., Fujita J.; | | | |
| RT | "Presence of alternative 5' untranslated sequences and identification | | | |
| RT | of cells expressing ctk transcripts in the brain and testis."; | | | |
| RL | Oncogene 10:945-952(1995). | | | |
| CC | -1- FUNCTION: COULD PLAY A SIGNIFICANT ROLE IN THE SIGNAL TRANSDUCTION | | | |
| CC | OR HEMATOPOIETIC CELLS. MAY REGULATE TYROSINE KINASE ACTIVITY OF | | | |
| CC | SRC-FAMILY MEMBERS IN BRAIN BY SPECIFICALLY PHOSPHORYLATING THEIR | | | |
| CC | C-TERMINAL REGULATORY TYROSINE RESIDUE WHICH ACTS AS A NEGATIVE | | | |
| CC | REGULATORY SITE. IT MAY PLAY AN INHIBITORY ROLE IN THE CONTROL OF | | | |
| CC | T-CELL PROLIFERATION. | | | |
| CC | -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein | | | |
| CC | tyrosine phosphate. | | | |
| CC | -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable). | | | |
| CC | -1- ALTERNATIVE PRODUCTS: | | | |
| CC | .Event-Alternative splicing; Named isoforms-2; | | | |
| CC | Name-1; | | | |
| CC | Isoid=P41242-1; Sequence=Displayed; | | | |
| CC | Name-2; | | | |
| CC | Isoid=P41242-2; Sequence=VSP_004966; | | | |
| CC | Note=Minor isoform: | | | |
| CC | -1- TISSUE SPECIFICITY: MOST ABUNDANT IN BRAIN, AND TO A LESSER EXTENT | | | |
| CC | IN THE SPLEEN, THE THYMUS AND THE LIVER. ALSO FOUND IN THE T-CELL | | | |
| CC | LINEAGE. | | | |
| CC | -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. CSK | | | |
| CC | SUBFAMILY. | | | |
| CC | -1- SIMILARITY: Contains 1 SH2 domain. | | | |
| CC | -1- SIMILARITY: Contains 1 SH3 domain. | | | |
| CC | ----- | | | |
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Db 359 SEDLVAKVSDFGIAKERRKLDSSRLPVKWTAEALKNGFSSKSDVMSGVILMEVFSY 418
QY 421 GRAPYPRKMSLKEVSEAVKGYRMEPPGCGPGPHVILMSQWEEAPARRPFRKLAETLAR 480
Db 419 GRAPYPRKMSLKEVSEAVKGYRMEPPDGCGRSVHTLMGSCWEAPARRPFRKLAETLAR 478
QY 481 ELRSAGAPASVSGQADGSTRPSQEP 507
Db 479 ELRSVGSAPAGQEAEGSAPTRSDP 505

RESULT 3
MATK_RAT
ID MATK_RAT STANDARD; PRT; 467 AA.
AC P41243;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Megakaryocyte-associated tyrosine-protein kinase (EC 2.7.1.112)
DE (Tyrosine-protein kinase CTK) (Protein kinase BAKK).
GN MATK OR CTK OR BAKK.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN-Sprague-Dawley; TISSUE=Hippocampus;
RX MEDLINE=95106341; PubMed=7807586;
RA Kuo S.S., Moran P., Grupp J., Armanini M., Phillips H.S., Goddard A.,
RA Casas I.W.;
RT "Identification and characterization of Bakt, a predominantly brain-
RT specific non-receptor protein tyrosine kinase related to Csk.";
RL J. Neurosci. Res. 38:705-715(1994).
CC -1- FUNCTION: COULD PLAY A SIGNIFICANT ROLE IN THE SIGNAL TRANSDUCTION
CC OF HEMATOPOIETIC CELLS. MAY REGULATE TYROSINE KINASE ACTIVITY OF
CC SRC-FAMILY MEMBERS IN BRAIN.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- TISSUE SPECIFICITY: ENRICHED IN LYMPHOID TISSUES.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. CSK
CC SUBFAMILY.
CC -1- SIMILARITY: Contains 1 SH2 domain.
CC -1- SIMILARITY: Contains 1 SH3 domain.
CC
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CC
CC EMBL, L34542; AAA64524.1; -.
CC PIR, I56579; I56579.
CC HSSP, P11362; IFGK.
CC InterPro: IPR000719; Prot_Kinase.
CC InterPro: IPR000980; SH2.
CC InterPro: IPR001452; SH3.
CC InterPro: IPR001245; Tyr_Pkinase.
CC Pfam: PF00069; pkinase; 1.
CC Pfam: PF00017; SH2; 1.
CC Pfam: PF00018; SH3; 1.
CC PRINTS: PR00401; SH2DOMAIN.
CC PRINTS: PR00109; TYRKINASE.
CC ProDom: PD000001; Prot_Kinase; 1.
CC SMART: SM00252; SH2; 1.
CC SMART: SM00326; SH3; 1.
CC SMART: SM00219; TYRK; 1.
CC PROSITE, PS00107; PROTEIN_KINASE_ATP; 1.

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DR PROSITE, PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE, PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE, PS50001; SH2; 1.
DR PROSITE, PS50002; SH3; 1.
KW transferase; Tyrosine-protein kinase; ATP-binding; SH2 domain;
KW SH3 domain; phosphorylation.
FT DOMAIN 22 69
FT DOMAIN 81 170
FT DOMAIN 194 443
FT NP_BIND 200 208
FT BINDING 221 221
FT ACT_SITE 311 311
SQ SEQUENCE 467 AA; 51896 MW; 283FE9348BB5FA8F CRC64;

Query Match 83.2%; Score 2221.5; DB 1; Length 467;
Best Local Similarity 89.3%; Pred. No. 2e-146;
Matches 417; Conservative 27; Mismatches 22; Indels 1; Gaps 1;

QY 42 MPTRRAPGTQCITCKCEHTRPKPELAFRKGDVVTILEACENKSWTVVHHSTGOGGLA 101
Db 1 MPTQRAWAPGTQCITCKCEHTRPKPELAFRKGDVVTILEACEDKSWTVRAKHHSSGOGGLA 60
QY 102 AGALRRERALSADPKSLMPHFHGTISGQAVVQLOPPEDGLFLVRESARHPDDYLCVS 161
Db 61 AALRRERALSADPKSLMPHFHGTISGQAVVQLOPPEDGLFLVRESARHPDDYLCVS 120
QY 162 FGRDVIHYRLHRDGLTIDEAVFCNLDMDVHYSKDGAICTKLVPRKRHGTSAE 221
Db 121 FGRDVIHYRLHRDGLTIDEAVFCNLDMDVHYRDKAICTKLVPRKRHGTSAE 180
QY 222 ELARAGMLNLQHLTLGAOIGEGEFGAVLOGEYLQKVAVKNIKCDVTQAFLDEFAVMT 281
Db 181 ELAKAGMLDLQHLTLGAOIGEGEFGAVLOGEYLQKVAVKNIKCDVTQAFLDEFAVMT 240
QY 282 KQHENVLYRLGTYLHOGIYIWEHNSKGLVFLTRGALVNTQQLQSLHVAEGH 341
Db 241 KQHENVLYRLGTYLHOGIYIWEHNSKGLVFLTRGALVNTQQLQSLHVAEGH 300
QY 342 YLESKRLVHRDLAARNILVSEDLVAVKVSDFGLAKAE-RKGLDSSRLPVKWTAEALKHK 400
Db 301 YLESKRLVHRDLAARNILVSEDLVAVKVSDFGLAKAEALKRLGDLSSRLPVKWTAEALKNG 360
QY 401 FTSKSPVMSFGVILMEVFSYGRAPYPRKMSLKEVSEAVKGYRMEPPGCGPHVILMSGC 460
Db 361 FTSKSPVMSFGVILMEVFSYGRAPYPRKMSLKEVSEAVKGYRMEPPDSCPGPHVILMSGC 420
QY 461 WEAEPRAPRPPFRKLAETLARLSAGAPASVSGQADGSTRPSQEP 507
Db 421 WEAEPRAPRPPFRKLAETLARLSAGAPASVSGQADGSTRPSQEP 467

RESULT 4
CSK_CHICK
ID CSK_CHICK STANDARD; PRT; 450 AA.
AC P41239;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tyrosine-protein kinase CSK (EC 2.7.1.112) (C-Src kinase).
GN CSK.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
ON NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92196083; PubMed=1372437;
RA Sabe H., Knudsen B., Okada M., Nada S., Nakagawa H., Hanafusa H.;
RT "Molecular cloning and expression of chicken C-terminal Src kinase:
RT lack of stable association with c-Src protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2190-2194(1992).

```


CC -1- FUNCTION: SPECIFICALLY PHOSPHORYLATES A TYROSINE ON THE SRC
 CC KINASE. THIS TYROSINE ACTS AS A NEGATIVE REGULATORY SITE.
 CC CAN ALSO ACT ON THE LYN AND FYN KINASES.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. CSK
 CC SUBFAMILY.
 CC -1- SIMILARITY: Contains 1 SH2 domain.
 CC -1- SIMILARITY: Contains 1 SH3 domain.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M85039; AAA51436.1; -;
 DR PIR; A41973; A41973.
 DR HSSP; P41240; ICSK.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR ProDom; PD000093; SH2; 1.
 DR ProDom; PD000066; SH3; 1.
 DR SMART; SM00325; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; TYRKC; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KM Transferase; Tyrosine-protein kinase; ATP-binding; SH2 domain;
 KM SH3 domain; Phosphorylation.
 FT DOMAIN 9 70
 FT DOMAIN 82 171 SH2.
 FT DOMAIN 195 450 SH3.
 FT NP_BIND 201 209 PROTEIN_KINASE.
 FT BINDING 222 222 ATP (BY SIMILARITY).
 FT ACT_SITE 314 314 BY SIMILARITY.
 FT MOD_RES 416 416 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 SQ SEQUENCE 450 AA; 50751 MW; 5AA3C406AA4F246F CRC64;
 Query Match 46.9%; Score 1253.5; DB 1; Length 450;
 Best Local Similarity 53.9%; Pred. No. 1.6e-79;
 Matches 234; Conservative 84; Mismatches 113; Indels 3; Gaps 2;
 QY 47 WAPETOCITCENTRPRKPELAERKGDVVTILEACENKSWYRVKHHNTSGEGILLAGALR 106
 DB 8 WPSSTECIAKYNFHGTAEODLFPSKGDVLTIVAVTKDPNNKAKNKV-GREGILPANYVQ 66
 QY 107 ERESLADPKLTSLMPWFGKTSISGEAVOQLPPEDGLFVRESARHGVDVLYCSFGRDV 166
 DB 67 KRESVKAGIKTSLMPWFGKTSISGEAVOQLPPEDGLFVRESARHGVDVLYCSFGRDV 126
 QY 167 IHYEVLRDGHILIDEAVFPCNLDMWVHSKDGALCTKLVKRRKHGTSAGEELARA 226
 DB 127 EHYIIISSTKSLIDEVYFENLMQVLEHTTDDGLCSRLIKRKVMEGYIAADERSRS 186
 QY 227 GWLNLQHLTGLAIOGEGFCAVLOGEYLQKVAVKIKCDVTAQAFLDETAVMTKQHE 286
 DB 187 GWALNMKDLKLLQIIGGEGFDVMDGYRGNKVAVKCIKNDATQAFLAEASVMTQLRHS 246

QY 287 NLVRLGLYLHO--GLIYMEVSKGNLVNPLRTGRALVNTAQLLOPSLHAGMEYLE 344
 DB 247 NLVOLLGIVYEKSGLLIYVETYMAGKSLVDLRSRGSVLDGDCILKSLVYCAAMEYLE 306
 QY 345 SKRLVHRDLARNILVSEDLVAKVSDGLAKERRGLDSSRLPVKWTAPALKHGKFTSK 404
 DB 307 ANNFVHRDLARNILVSEDLVAKVSDGLAKERRGLDSSRLPVKWTAPALKHGKFTSK 366
 QY 405 SDVMSFGVLLMEVSYGRAPPKMSLKEVSAVEKGRMEPECCPGFVHYVLMSGCAE 464
 DB 367 SDVMSFGVLLMEVSYGRAPPKMSLKEVSAVEKGRMEPECCPGFVHYVLMSGCAE 426
 QY 465 PARPPPKLAELK 478
 DB 427 PGRHPSFQHLREQL 440
 RESULT 5
 CSK_HUMAN
 ID CSK_HUMAN STANDARD; PRT: 450 AA.
 AC P41240.
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tyrosine-protein kinase CSK (EC 2.7.1.112) (C-SRC kinase) (Protein-
 DE tyrosine kinase CYL).
 GN CSK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_Taxid:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-93241739; PubMed-7683131;
 RA Breuninger A., Karn T., Strebhardt K., Ruebsamen-Waigmann H.;
 RT "Characterization of the human CSK locus.";
 RL Oncogene 8:1365-1369(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-92050797; PubMed-1945408;
 RA Partanen J., Armstrong E., Bergman M., Maekelae T.P., Hirvonen H.,
 RA Huebner K., Allitalo K.;
 RT "CYL encodes a putative cytoplasmic tyrosine kinase lacking the
 RT conserved tyrosine autophosphorylation site (Y416src).";
 RL Oncogene 6:2013-2018(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX TISSUE-Lung;
 RC MEDLINE-92073297; PubMed-1720539;
 RA Breuninger A., Holtrich U., Strebhardt K., Ruebsamen-Waigmann H.;
 RT "Two additional protein-tyrosine kinases expressed in human lung;
 RT fourth member of the fibroblast growth factor receptor family and an
 RT intracellular protein-tyrosine kinase.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:10411-10415(1991).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 1-71.
 RX MEDLINE-94185778; PubMed-7511113;
 RA Borchert T.V., Mathieu M., Zeelen J.P., Courtneidge S.A.,
 RA Wierenga R.K.;
 RT "The crystal structure of human CSKSH3: structural diversity near the
 RT RT-Src and p-Src loop.";
 RL FEBS Lett. 341:79-85(1994).
 CC -1- FUNCTION: SPECIFICALLY PHOSPHORYLATES A TYROSINE ON THE SRC
 CC KINASE. THIS TYROSINE ACTS AS A NEGATIVE REGULATORY SITE.
 CC CAN ALSO ACT ON THE LYN AND FYN KINASES.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. CSK
 CC SUBFAMILY.
 CC -1- SIMILARITY: Contains 1 SH2 domain.
 CC -1- SIMILARITY: Contains 1 SH3 domain.

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CC EMBL: X58631; CAA41484.1; -
 DR PDB: 1K59A; 01-MAY-02.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001245; Tyr_Pkinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR PRINTS: PR00109; TYRKINASE.
 DR Prodom: PD000001; Prot_kinase; 1.
 DR Prodom: PD000093; SH2; 1.
 DR Prodom: PD000066; SH3; 1.
 DR SMART: SM00326; SH2; 1.
 DR SMART: SM00326; SH3; 1.
 DR SMART: SM00219; TYRKC; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS50002; SH3; 1.
 DR Transferrase: Tyrosine-protein kinase; ATP-binding; SH2 domain;
 KW SH3 domain; Phosphorylation; 3D-structure.
 FT DOMAIN 9 70
 FT DOMAIN 82 171 SH2.
 FT DOMAIN 195 445 PROTEIN_KINASE.
 FT NP_BIND 201 209 ATP (BY SIMILARITY).
 FT BINDING 222 222 ATP (BY SIMILARITY).
 FT ACT_SITE 314 314 BY SIMILARITY.
 FT MOD_RES 416 416 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 SQ SEQUENCE 450 AA; 50746 MW; 393DC8D737DAC67A CRC64;

Query Match 46.5%; Score 1242.5; DB 1; Length 450;
 Best Local Similarity 54.1%; Pred. No. 9,4e-79;
 Matches 235; Conservative 81; Mismatches 115; Indels 3; Gaps 2;

QY 47 WAPGTCITRCENTHPRPGLAEKRGDVITILECENKSWYRVKHNHTSGEGLLAAGLR 106
 DB 8 WPSGTECIARYKNFNGHTAEODLPFCCKGDVLTIVAVTKDPNMYKAKNKV-GREGIIPANVY 66
 QY 107 ERELSADPRLSLMPWPHGKISGGEAVOQLPPEDGLFVRESNRHGEDVYLCYSGRDY 166
 DB 67 KREGVKAQTKLSLMPWPHGKITRQARLLYPPETGLFVRESNTPYGDYTLCVSCGKY 126
 QY 167 IHYVFLHRDGLTIDEAVFCNLDVNEHYSKDGALCTKLVPRKRHGTSADEELARA 226
 DB 127 EHYIMYHASKLSIDEVEYFENLMQVLEHTTDDAGCTRLIKRKNVEGYAODEYRYS 186
 QY 227 GMLNLQHLTGAQIGGEFGAVLQGEYLGOKYAVNKKICDVTAAQLDETVAMTKQHE 286
 DB 187 GMLNLMKELKLTQITGGEFGDVALGDRGNKVAVKCIKNDAQAFLAEASVNTOLRHS 246
 QY 287 NLVALLGVIIHQ--GLTIYVNEHYSKGLVNFRLTRGALVNTADLLOPSLHVAAGMEYLE 344
 DB 247 NLVOLLGVIVEEKGLTIYVEYMAKGLVLDLRSRGSVYLGDDLLRFLSDVCCAMEYLE 306
 QY 345 SKRLVHRDLAARNLVSEEDIVAKVSDFGLAKEKGLDSSRLPYKWTAPALKIGKFTSK 404
 DB 307 GNNRVHHDLAARNLVSEEDIVAKVSDGLTRKASSTQDTGTLPKWTAPALRKRKSTK 366
 QY 405 SDVWSFGVLLMEVFSYGRAPYPKMSLKEVSEAVEKGYRMEPECCPGPVHVMSSCWEAE 464
 DB 367 SDVWSFGVLLMEVFSYGRAPYPRIPKDVVPRVEKGYKMDAPDCPPAVYDVMAKNCWILD 426
 QY 465 PARPPPRKLAELK 478
 DB 427 AATRPFLQLEKREL 440

RESULT 7

CSK_MOUSE
 ID CSK_MOUSE STANDARD; PRT; 450 AA.
 AC P41241; 003143; 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tyrosine-protein kinase CSK (EC 2.7.1.112) (C-SRC kinase) (Protein-tyrosine kinase MPR-2).
 GN CSK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=94195789; PubMed=7511815;
 RA Klages S., Adam D., Class K., Fargnoli J., Bolen J.B., Penhallow R.C.;
 RT "Csk: a protein-tyrosine kinase related to Csk that defines an enzyme family.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:2597-2601(1994).
 [2]
 RP SEQUENCE OF 316-367 FROM N.A.
 RC SRRAIN-C57BL/6; TISSUE=Embryonic brain;
 RX MEDLINE=9306484; PubMed=1281307;
 RA Gliardi-Hebenstreit P., Nieto M.A., Fraaij M., Mattei M.-G., Chestier A., Wilkinson D.G., Charney P.;
 RT "An Eph-related receptor protein tyrosine kinase gene segmentally expressed in the developing mouse hindbrain.";
 RL Oncogene 7:2499-2506(1992).
 CC -1- FUNCTION: SPECIFICALLY PHOSPHORYLATES A TYROSINE ON THE SRC KINASE. THIS TYROSINE ACTS AS A NEGATIVE REGULATORY SITE.
 CC CAN ALSO ACT ON THE LYN AND FYN KINASES.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine -> ADP + protein tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 CC -1- TISSUE SPECIFICITY: UNIQUTOUS, BUT MOST ABUNDANT IN THYMUS AND SPLEEN, AS WELL AS IN NEONATAL BRAIN.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. CSK SUBFAMILY.
 CC -1- SIMILARITY: Contains 1 SH2 domain.
 CC -1- SIMILARITY: Contains 1 SH3 domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL: U05247; AAA18766.1; -
 DR EMBL: X57242; CAA40518.1; -
 DR PIR: I48929; I48929.
 DR PDB: 1JEG; 31-OCT-01.
 DR MGD: MGI:88337; CSK.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001245; Tyr_Pkinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR PRINTS: PR00109; TYRKINASE.
 DR Prodom: PD000001; Prot_kinase; 1.
 DR Prodom: PD000093; SH2; 1.
 DR Prodom: PD000066; SH3; 1.
 DR SMART: SM00326; SH2; 1.
 DR SMART: SM00326; SH3; 1.

[illegible]

| RESULT 9 | STANDARD; | PRT; | 508 AA. |
|----------|---|------|---------|
| AC ID | LCK_MOUSE | | |
| DT | P06240; Q61794; Q61795; Q62320; | | |
| DT | 01-JAN-1988 (Rel. 06, Created) | | |
| DT | 01-FEB-1994 (Rel. 28, Last sequence update) | | |
| DT | 28-FEB-2003 (Rel. 41, Last annotation update) | | |
| DE | Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (P56-LCK) (LCK). | | |
| DE | LCK OR LSK-T. | | |
| GN | LCK OR LSK-T. | | |
| OC | Mus musculus (Mouse). | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | |
| OX | NCBI_TaxID-10090; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RX | MEDLINE-86079521; Pubmed-2416464; | | |
| RT | RA Math J.D., Peet R., Krebs E.G., Perlmutter R.M.; | | |
| RL | "A lymphocyte-specific protein-tyrosine kinase gene is rearranged and overexpressed in the murine T cell lymphoma L5178." | | |
| RL | Cell 43:393-404(1985). | | |
| RN | [2] | | |
| RP | SEQUENCE FROM N.A. | | |
| RX | MEDLINE-86146842; Pubmed-3081813; | | |
| RT | Voronova A.F., Sefton B.M.; | | |
| RL | "Expression of a new tyrosine kinase is stimulated by retrovirus promoter insertion." | | |
| RL | Nature 319:682-685(1986). | | |
| RN | [3] | | |
| RP | SEQUENCE OF 1-34 FROM N.A. | | |
| RX | MEDLINE-89096891; Pubmed-2850479; | | |
| RT | Gavrin A.M., Pawar S., Marth J.D., Perlmutter R.M.; | | |
| RL | "Structure of the murine lck gene and its rearrangement in a murine lymphoma cell line." | | |
| RL | Mol. Cell. Biol. 8:3058-3064(1988). | | |
| RN | [4] | | |
| RP | SEQUENCE OF 1-10 FROM N.A. | | |
| RX | MEDLINE-88142832; Pubmed-3501824; | | |
| RT | Voronova A.F., Adler H.T., Sefton B.M.; | | |

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CC -----

CC -1- SIMILARITY: Contains 1 SH2 domain.

CC -1- SIMILARITY: Contains 1 SH domain.

CC -----

CC SUBFAMILY.

CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC

CC T-CELL ONTOGENY.

CC -1- DEVELOPMENTAL STAGE: LEVELS REMAIN RELATIVELY CONSTANT THROUGHOUT

CC AT AN ELEVATED LEVEL IN LSTRA AND THY 19 (T-CELL LYMPHOMA) CELLS.

CC -1- TISSUE SPECIFICITY: PRESENT AT A LOW LEVEL IN MOST T CELLS, AND

CC CM4 OR CB8.

CC -1- SUBCELLULAR LOCATION: BOUND TO THE CYTOPLASMIC DOMAIN OF EITHER

CC tyrosine phosphate.

CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein

CC DEVELOPMENT.

CC ITS EARLY EXPRESSION IS ESSENTIAL FOR EARLY T-LYMPHOCYTE

CC BIOCHEM. J. 303:749-753(1994).

CC -1- FUNCTION: MAY PARTICIPATE IN ANTIGEN-INDUCED T-CELL ACTIVATION.

CC PALMITOYLATION.

CC MEDLINE-95071286; PubMed-7980442.

CC RA Koegl M., Zlatkine P., Ley S.C., Courtneidge S.A., Magee A.I.;

CC RT "Palmitoylation of multiple Src-family kinases at a homologous N-

CC RL terminal motif";

CC [11] Mol. Cell. Biol. 13:6385-6392(1993).

CC [10]

CC PALMITOYLATION.

CC MEDLINE-94019312; PubMed-8413237;

CC RA Shenoy-Scaria A.M., Timson L.K., Kwong J., Shaw A.S., Lublin D.M.;

CC RT "The conserved lysine of the catalytic domain of protein kinases is

CC RT actively involved in the phosphotransfer reaction and not required

CC RT for anchoring ATP.";

CC Proc. Natl. Acad. Sci. U.S.A. 90:442-446(1993).

CC [9]

CC MUTAGENESIS.

CC MEDLINE-93133805; PubMed-8421674;

CC RA Carrera A.C., Alexandrov K., Roberts T.M.;

CC RT "The conserved lysine of the catalytic domain of protein kinases is

CC RT actively involved in the phosphotransfer reaction and not required

CC RT for anchoring ATP.";

CC Proc. Natl. Acad. Sci. U.S.A. 88:3977-3981(1991).

CC [8]

CC MUTAGENESIS OF TYR-504.

CC MEDLINE-91219495; PubMed-1708890;

CC RA Abraham K.M., Levin S.D., Marsh J.D., Forbush K.A., Perlmutter R.M.;

CC RT "Tyrosine tumorigenesis induced by overexpression of p56lck.";

CC Proc. Natl. Acad. Sci. U.S.A. 88:3977-3981(1991).

CC [7]

CC MUTAGENESIS OF LYS-272.

CC MEDLINE-91163633; PubMed-1706070;

CC RA Abraham N., Miceli M.C., Parnes J.C., Veilleux A.;

CC RT "Enhancement of T-cell responsiveness by the lymphocyte-specific

CC RT tyrosine protein kinase p56lck.";

CC Nature 350:62-66(1991).

CC [6]

CC MUTAGENESIS.

CC MEDLINE-93059694; PubMed-1279202;

CC RA Hurley T.R., Amrein K.E., Sefton B.M.;

CC RT "Creation and characterization of temperature-sensitive mutants of

CC RT the lck tyrosine protein kinase.";

CC J. Virol. 66:7406-7413(1992).

CC [5]

CC MUTAGENESIS OF TYR-504.

CC MEDLINE-88248001; PubMed-3380790;

CC RA Amrein K.E., Sefton B.M.;

CC RT "Avian reovirus mRNAs are nonfunctional in infected mouse cells:

CC RT transnational basis for virus host-range restriction.";

CC Proc. Natl. Acad. Sci. U.S.A. 85:4257-4261(1988).

CC [4]

CC "Two lck transcripts containing different 5' untranslated regions are

CC RT present in T cells.";

CC Mol. Cell. Biol. 7:4407-4413(1987).

CC [3]

CC MUTAGENESIS OF TYR-504.

CC MEDLINE-88248001; PubMed-3380790;

CC RA Amrein K.E., Sefton B.M.;

CC RT "Avian reovirus mRNAs are nonfunctional in infected mouse cells:

CC RT transnational basis for virus host-range restriction.";

CC Proc. Natl. Acad. Sci. U.S.A. 85:4257-4261(1988).

CC [2]

CC "Two lck transcripts containing different 5' untranslated regions are

CC RT present in T cells.";

CC Mol. Cell. Biol. 7:4407-4413(1987).

CC [1]

RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Leukemic T-cell;
RX MEDLINE=96085119; PubMed=7495859;
RA Vogel L.B., Arthur R., Fujita D.J.;
RT "An aberrant lck mRNA in two human T-cell lines.";
RL Biophys. Acta 1264:168-172(1995).
[6]
RN SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins B.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Heiton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[7]
RN SEQUENCE OF 13-508 FROM N.A.
RC TISSUE=Peripheral blood lymphocytes;
RX MEDLINE=20462621; PubMed=11009087;
RA Boncristiano M., Majolini M.B., D'Elia M.M., Pacini S., Valensin S.,
RA Olivieri C., Amedei A., Falini B., Del Prete G., Telford J.L.,
RA Balderi C.T.;
RT "Defective recruitment and activation of ZAP-70 in common variable
RT immunodeficiency patients with T cell defects.";
RL Eur. J. Immunol. 30:2632-2638(2000).
[8]
RN SEQUENCE OF 367-508 FROM N.A.
RX MEDLINE=88217332; PubMed=2835736;
RA Veillette A., Foss F.M., Sausville E.A., Bolen J.B., Rosen N.;
RT "Expression of the lck tyrosine kinase gene in human colon carcinoma
RT and other non-lymphoid human tumor cell lines.";
RL Oncogene Res. 1:357-374(1987).
[9]
RN SEQUENCE OF 374-508 FROM N.A.
RX MEDLINE=87000726; PubMed=3489486;
RA Trevillian J.M., Lin Y., Chen S.J., Phillips C.A., Canna C.,
RA Lima T.J.;
RT "Human T lymphocytes express a protein-tyrosine kinase homologous to
RT p56lck.";
RL Biochim. Biophys. Acta 888:286-295(1986).
[10]
RN SEQUENCE OF 1-34 FROM N.A.
RX MEDLINE=89096891; PubMed=2850479;
RA Garvin A.M., Pawar S., Martin J.D., Perlmutter R.M.;
RT "Structure of the murine lck gene and its rearrangement in a murine
RT lymphoma cell line.";
RL Mol. Cell. Biol. 8:3058-3064(1988).
[11]
RN SEQUENCE OF 1-34 FROM N.A.
RX MEDLINE=89313764; PubMed=2787474;
RA Takadera T., Leung S., Gernone A., Koga Y., Takihara Y.,
RA Miyamoto N.G., Mak T.W.;
RT "Structure of the two promoters of the human lck gene: differential
RT accumulation of two classes of lck transcripts in T cells.";
RL Mol. Cell. Biol. 9:2173-2180(1989).
[12]
RN MASS SPECTROMETRY.
RC TISSUE=Breast cancer;
RX MEDLINE=21829512; PubMed=11840567;
RA Harris R.A., Yang A., Stein R.C., Lucy K., Brusten T., Herath A.,
RA Parekh R., Waterfield M.D., O'Hare M.D., Neville M.A., Page M.J.,
RA Zvelebil M.J.;
RT "Cluster analysis of an extensive human breast cancer cell line
RT protein expression map database.";
RL Proteomics 2:212-223(2002).
[13]
RN INTERACTION WITH PI3K.
RX MEDLINE=94067101; PubMed=7504174;
RA Vogel L.B., Fujita D.J.;
RT "The SH3 domain of p56lck is involved in binding to
RT phosphatidylinositol 3'-kinase from T lymphocytes.";
RL Mol. Cell. Biol. 13:7408-7417(1993).
[14]
RN INTERACTION WITH KHDRSL.
RX MEDLINE=95155308; PubMed=7852312;
RA Vogel L.B., Fujita D.J.;
RT "p70 phosphorylation and binding to p56lck is an early event in
RT interleukin-2-induced onset of cell cycle progression in
RT T-lymphocytes.";
RL J. Biol. Chem. 270:2506-2511(1995).
[15]
RN PHOSPHORYLATION OF TYR-504.
RX MEDLINE=92347326; PubMed=1639064;
RA Bergman M., Mustelin T., Oetken C., Partanen J., Flint N.A.,
RA Amrein K.E., Altero M., Burn P., Altalo K.;
RT "The human p50csk tyrosine kinase phosphorylates p56lck at Tyr-505 and
RT down regulates its catalytic activity.";
RL EMBO J. 11:2919-2924(1992).
[16]
RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 52-225.
RX MEDLINE=94203291; PubMed=7512222;
RA Eck M.J., Atweell S.K., Shoelson S.E., Harrison S.C.;
RT "Structure of the regulatory domains of the Src-family tyrosine
RT kinase Lck.";
RL Nature 368:764-769(1994).
[17]
RN X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 126-220.
RX MEDLINE=95173978; PubMed=7532720;
RA Mikol V., Baumann G., Keller T.H., Manning U.M., Zurini M.G.M.;
RT "The crystal structures of the SH2 domain of p56lck complexed with
RT two phosphopeptides suggest a gated peptide binding site.";
RL J. Mol. Biol. 246:344-355(1995).
[18]
RN X-RAY CRYSTALLOGRAPHY (1.0 ANGSTROMS) OF 121-225.
RX MEDLINE=96177765; PubMed=8604142;
RA Tong L., Warren T.C., King J., Betageri R., Rose J., Jakes S.;
RT "Crystal structures of the human p56lck SH2 domain in complex with
RT two short phosphotyrosyl peptides at 1.0-A and 1.8-A resolution.";
RL J. Mol. Biol. 256:601-610(1996).
[19]
RN X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 118-225.
RX MEDLINE=98352059; PubMed=9685372;
RA Tong L., Warren T.C., Lukas S., Schembri-King J., Betageri R.,
RA Proudfoot J.R., Jakes S.;
RT "Carboxymethyl-phenylalanine as a replacement for phosphotyrosine in
RT SH2 domain binding.";
RL J. Biol. Chem. 273:20238-20242(1998).
[20]
RN X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 230-500.
RX MEDLINE=97100952; PubMed=8945479;
RA Yamaguchi H., Hendrickson W.A.;
RT "Structural basis for activation of human lymphocyte kinase Lck upon
RT tyrosine phosphorylation.";
RL Nature 384:484-489(1996).
[21]
RN -1- FUNCTION: MAY PARTICIPATE IN ANTIGEN-INDUCED T-CELL ACTIVATION.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
CC tyrosine phosphate.
CC -1- SUBUNIT: Binds to phosphatidylinositol 3'-kinase (PI3K) from T
CC lymphocytes through its SH3 domain and to the tyrosine
CC phosphorylated form of KHDRSL/p70 through its SH2 domain.
CC -1- SUBCELLULAR LOCATION: BOUND TO THE CYTOPLASMIC DOMAIN OF EITHER

| | | | | | | | |
|----|----------|------|-----|-------|-----|---------------------------|--------|
| 50 | SEQUENCE | 526 | AA; | 58953 | MM; | 85D356HBBCB14D | CRC64; |
| FT | DOMAIN | 81 | | 142 | | SH3. | |
| FT | DOMAIN | 148 | | 245 | | SH3. | |
| FT | DOMAIN | 267 | | 517 | | PROTEIN KINASE. | |
| FT | NP_BIND | 273 | | 281 | | ATP (BY SIMILARITY). | |
| FT | BINDING | 295 | | 295 | | ATP (BY SIMILARITY). | |
| FT | ACT_SITE | 386 | | 386 | | BY SIMILARITY. | |
| FT | MOD_RES | 416 | | 416 | | PHOSPHORYLATION (AUTO-). | |
| FT | CONFLICT | 10 | | 10 | | G -> D (IN REF. 2 AND 3). | |
| FT | CONFLICT | 63 | | 63 | | D -> G (IN REF. 2). | |
| FT | CONFLICT | 96 | | 96 | | I -> T (IN REF. 3). | |
| FT | CONFLICT | 124 | | 124 | | V -> L (IN REF. 2). | |
| FT | CONFLICT | 301 | | 301 | | T -> N (IN REF. 3). | |
| FT | CONFLICT | 320 | | 320 | | K -> E (IN REF. 2 AND 3). | |
| FT | CONFLICT | 496 | | 496 | | S -> C (IN REF. 2 AND 3). | |
| FT | TURN | 147 | | 148 | | | |
| FT | STRAND | 149. | | 151 | | | |
| FT | HELIX | 155 | | 162 | | | |
| FT | TURN | 163 | | 163 | | | |
| FT | TURN | 165 | | 166 | | | |
| FT | TURN | 169 | | 170 | | | |
| FT | STRAND | 172. | | 176 | | | |
| FT | TURN | 181 | | 182 | | | |
| FT | STRAND | 184 | | 192 | | | |
| FT | TURN | 193 | | 195 | | | |
| FT | STRAND | 196 | | 206 | | | |
| FT | TURN | 208 | | 209 | | | |
| FT | STRAND | 212 | | 213 | | | |
| FT | TURN | 216 | | 217 | | | |
| FT | STRAND | 219 | | 220 | | | |
| FT | HELIX | 223 | | 230 | | | |
| FT | TURN | 231 | | 232 | | | |
| FT | TURN | 235 | | 246 | | | |
| FT | STRAND | 244 | | 244 | | | |

OY 66 ELAFRKGDVVTLLEACENKSWRYVHNHTSGOGLLAAGLAREALSLADPKLSIMPWFHG 125
:
Db 99 DLSRKGGRLDINNTEG--NMWLNHSYTTGGQGYIPSNVAUSDSTJQAE-----EWTYG 151

OY 126 KISGOGAQQLOAPED--GLFLVRESARHPGDVLYCVS----FGRDVIHYRVLRHD-GH 177
:
Db 152 KITRESERLLINPENPGTFLVRESETTKGAYCLSVSDFNAGKNVHYXIRKLDSGG 211

OY 178 LTIDEAVFCUMLDMWEHYHNSDKGALCTIKL--VRKRKHGTSAEEELARAQGLNLNQL 235
:
Db 212 FYITSRFQSSQQQLVAVYSKRAQDLCHRLTNVCPTSKQTQG---LAKDMAEIPIRESL 267

```

RESULT 12
SRC_AVISS
ID SRC_AVISS STANDARD; PRT; 568 AA.
AC P14084;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tyrosine-protein kinase transforming protein SRC (EC 2.7.1.112) (P60-
DE SRC).
DE V-SRC.
GN Avian sarcoma virus (strain S1).
OS Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.
OX NCBI_TaxID=11881;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=87064539; Pubmed=3097513;
RA Ikwa S., Hagino-Yamagishi K., Kawai S., Yamamoto T., Toyoshima K.;
"Activation of the cellular src gene by transducing retrovirus.";
RL Mol. Cell. Biol. 6:2420-2428(1986).
RT -1- FUNCTION: THIS PHOSPHOPROTEIN, REQUIRED FOR BOTH THE INITIATION
CC AND THE MAINTENANCE OF NEOPLASTIC TRANSFORMATION, IS A PROTEIN
CC KINASE THAT CATALYZES THE PHOSPHORYLATION OF TYROSINE RESIDUES
CC IN VITRO.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
CC SUBFAMILY.
CC -1- SIMILARITY: Contains 1 SH2 domain.
CC PIR: A25375; TVFVSL.
DR HSSP: P00523; 2PTK.
DR InterPro: IPR000719; Prot_Kinase.
DR InterPro: IPR000980; SH2.
DR InterPro: IPR001452; SH3.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00069; kinase; 1.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00018; SH3; 1.
DR PRINTS: PR00401; SH2DOMAIN.
DR PRINTS: PR00452; SH3DOMAIN.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Prot_kinase; 1.
DR ProDom: PD000093; SH2; 1.
DR ProDom: PD000066; SH3; 1.
DR SMART: SM00352; SH2; 1.
DR SMART: SM00326; SH3; 1.
DR SMART: SM00219; TYK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PSS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PSS0001; SH2; 1.
DR PROSITE: PSS0002; SH3; 1.

```

Tyrosine-protein kinase; Oncogene; Transferase; Phosphorylation;
 KW ATP-binding; Myristate; SH3 domain; SH2 domain.
 FT LIPID 2 2 MYRISTATE.
 FT DOMAIN 81 142 SH3.
 FT DOMAIN 148 245 SH2.
 FT DOMAIN 267 520 PROTEIN KINASE.
 FT NP_BIND 273 281 ATP (BY SIMILARITY).
 FT BINDING 295 295 ATP (BY SIMILARITY).
 FT ACT_SITE 386 386 BY SIMILARITY.
 FT MOD_RES 416 416 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 SQ SEQUENCE 568 AA: 63632 MW: 13777DB121F70998 CRC64;
 Query Match 27.5%; Score 734.5; DB 1; Length 568;
 Best Local Similarity 39.5%; Pred. No. 1.7e-43;
 Matches 168; Conservative 75; Mismatches 155; Indels 27; Gaps 10;
 QY 66 ELAFKRGDVYVTLLEACENKSWYRVKHHNSGQGLLAAGLRERALSADPKLSMPWFG 125
 DB 99 DLSFKKGERLQIVNNTEG--DWWLHSLTGTGTGTPSNYVADSDSIQAE-----EWFVG 151
 QY 126 KISGOEAVOQLOPPED--GLFLVRESARHPGDIYLCVS-----FGRDVHYHYLRHD--GH 177
 DB 152 KITRRESERLLNPNRPCTFLVRESEETTKGAYCLSDPDNAKGILNVKHYIKRLDSGG 211
 QY 178 LTIIDEAVFPCNLMDEYHSKDKGAICTYL--VRPKRHGTSAEELARAGMLNLQHL 235
 DB 212 FYITSRTQPSLSQQLVAVYSKHAADGICHLTIVNCPTSKPQTGG---LAKDMEIPRESL 267
 QY 236 TLGAOIGEGFAGVLOGEYLG--OKYAAVKNIK--CDVTAQAFIDETAVMTKMHENLVRLIG 293
 DB 268 RLEVKLGQCCFGEVMMGTWNGTTRVAIKTLKPGTMSPEAFLOEAOVMKLRHEKILVLYA 327
 QY 294 VILHOGLYIVMHSVSKGNLVNFLRTGRALVNTAQLDQSLVNAEGMEYLSKILVHRDL 353
 DB 328 VVSEEPYIVTEYMSKSLDLEFKGEMGYRLPOLVDAAQIASGMAYVERNNYVHRDL 387
 QY 354 AARNILVSDLYAKYSDDEGLAKA----ERKGDSSRLPVKWTAPALAKGFTSKSDVMS 409
 DB 388 RAANILVGNLVCKYADDEGLALIEDNETAAGAFPIKWTAPALAKGFTSKSDVMS 447
 QY 410 FGVLLMEVFSYGRAPPKMSLKEVSEAVEKGYRMEPECCPGPVHVLSSMCWEAPARP 469
 DB 448 FGIILLTELTTKGRVYPRGAVNREYLDQYRGYRMPCCPESLHLMQCKRKPDEERP 507
 QY 470 PERKL 474
 DB 508 TEYL 512
 RESULT 13
 SRC_AVIST STANDARD; PRT; 557 AA.
 AC P14085;
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase transforming protein SRC (BC 2.7.1.112) (P60-
 DE SRC).
 GN V-SRC.
 OS Avian sarcoma virus (strain S2).
 OC Viruses; Retroviral viruses; Retroviridae; Avian type C retroviruses.
 ON NCBI_TaxID=11882;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87064539; PubMed=3097513;
 RA Ikawa S., Hagino-Yamagishi K., Kawai S., Yamamoto T., Toyoshima K.,
 RT "Activation of the cellular src gene by transducing retrovirus.",
 RL Mol. Cell. Biol. 6:2420-2428(1986).
 CC -I- FUNCTION: THIS PHOSPHOPROTEIN, REQUIRED FOR BOTH THE INITIATION
 CC AND THE MAINTENANCE OF NEOPLASTIC TRANSFORMATION, IS A PROTEIN
 CC KINASE THAT CATALYZES THE PHOSPHORYLATION OF TYROSINE RESIDUES
 CC IN VITRO.
 CC -I- CATALYTIC ACTIVITY: ATP + a protein tyrosine -> ADP + protein

tyrosine phosphate.
 CC -I- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC -I- SIMILARITY: Contains 1 SH2 domain.
 CC -I- SIMILARITY: Contains 1 SH3 domain.
 DR PIR: B25375; TVFVS2.
 DR HSSP: P00523; ZPTK.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR ProDom: PD000093; SH2; 1.
 DR ProDom: PD000066; SH3; 1.
 DR SMART: SM00252; SH2; 1.
 DR SMART: SM00252; SH3; 1.
 DR SMART: SM00219; TyrKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 KW Tyrosine-protein kinase; Oncogene; Transferase; Phosphorylation;
 KW ATP-binding; Myristate; SH3 domain; SH2 domain.
 FT LIPID 2 2 MYRISTATE.
 FT DOMAIN 81 142 SH3.
 FT DOMAIN 148 245 SH2.
 FT DOMAIN 267 520 PROTEIN KINASE.
 FT NP_BIND 273 281 ATP (BY SIMILARITY).
 FT BINDING 295 295 ATP (BY SIMILARITY).
 FT ACT_SITE 386 386 BY SIMILARITY.
 FT MOD_RES 416 416 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 SQ SEQUENCE 557 AA: 62582 MW: BCC2A04CB99CEAFE CRC64;
 Query Match 27.5%; Score 734; DB 1; Length 557;
 Best Local Similarity 38.2%; Pred. No. 1.8e-43;
 Matches 175; Conservative 78; Mismatches 177; Indels 28; Gaps 11;
 QY 66 ELAFKRGDVYVTLLEACENKSWYRVKHHNSGQGLLAAGLRERALSADPKLSMPWFG 125
 DB 99 DLSFKKGERLQIVNNTEG--DWWLHSLTGTGTGTPSNYVADSDSIQAE-----EWFVG 151
 QY 126 KISGOEAVOQLOPPED--GLFLVRESARHPGDIYLCVS-----FGRDVHYHYLRHD--GH 177
 DB 152 KITRRESERLLNPNRPCTFLVRESEETTKGAYCLSDPDNAKGILNVKHYIKRLDSGG 211
 QY 178 LTIIDEAVFPCNLMDEYHSKDKGAICTYL--VRPKRHGTSAEELARAGMLNLQHL 235
 DB 212 FYITSRTQPSLSQQLVAVYSKHAADGICHLTIVNCPTSKPQTGG---LAKDMEIPRESL 267
 QY 236 TLGAOIGEGFAGVLOGEYLG--OKYAAVKNIK--CDVTAQAFIDETAVMTKMHENLVRLIG 293
 DB 268 RLEVKLGQCCFGEVMMGTWNGTTRVAIKTLKPGTMSPEAFLOEAOVMKLRHEKILVLYA 327
 QY 294 VILHOGLYIVMHSVSKGNLVNFLRTGRALVNTAQLDQSLVNAEGMEYLSKILVHRDL 353
 DB 328 VVSEEPYIVTEYMSKSLDLEFKGEMGYRLPOLVDAAQIASGMAYVERNNYVHRDL 387
 QY 354 AARNILVSDLYAKYSDDEGLAKA----ERKGDSSRLPVKWTAPALAKGFTSKSDVMS 409
 DB 388 RAANILVGNLVCKYADDEGLALIEDNETAAGAFPIKWTAPALAKGFTSKSDVMS 447
 QY 410 FGVLLMEVFSYGRAPPKMSLKEVSEAVEKGYRMEPECCPGPVHVLSSMCWEAPARP 469
 DB 448 FGIILLTELTTKGRVYPRGAVNREYLDQYRGYRMPCCPESLHLMQCKRKPDEERP 507
 QY 470 PERKLAELAR--SAGAPASVSGDADGDSISPSQE 506

DB 508 TFEYLAFLIEDYGLIAMTPMEDKQEGPRGETASNKOE 545

RESULT 14

SRC_CHICK

ID SRC_CHICK STANDARD; PRT: 532 AA.

AC P00523; Q90992; Q91343; Q91345; Q92013; Q98915;

DT 21-JUL-1986 (Rel. 01, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Proto-oncogene tyrosine-protein kinase Src (EC 2.7.1.112) (p60-Src) (c-Src).

GN SRC.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=83155664; PubMed=6299580;

RA Takeya T., Hanafusa H.;

RT "Structure and sequence of the cellular gene homologous to the RSV src gene and the mechanism for generating the transforming virus.";

RL Cell 32:881-890(1983).

RN [2]

RP REVISION TO 525.

RA Takeya T., Hanafusa H.;

RL Cell 34:319-319(1983).

RN [3]

RP SEQUENCE FROM N.A., AND PHOSPHORYLATION OF TYR-415 AND TYR-435.

RX MEDLINE=97008971; PubMed=8856081.

RA Weijland A., Neubauer G., Countinidge S.A., Mann M., Wierenga R.K., Superti-Furga G.;

RT "The purification and characterization of the catalytic domain of Src expressed in Schizosaccharomyces pombe. Comparison of unphosphorylated and tyrosine phosphorylated species.";

RL Eur. J. Biochem. 240:756-764(1996).

RN [4]

RP SEQUENCE OF 1-18 AND 484-533 FROM N.A.

RX MEDLINE=91304409; PubMed=1712905;

RA Dostal T., Levy J.B., Kang L., Brugge J.S., Wang L.H.;

RT "Analysis of CDNA's of the proto-oncogene c-src: heterogeneity in 5' exons and possible mechanism for the genesis of the 3' end of v-src.";

RL Mol. Cell. Biol. 11:4165-4176(1991).

RN [5]

RP ATP-BINDING SITE.

RX MEDLINE=84270751; PubMed=6431300;

RA Kamps M.P., Taylor S.S., Sefton B.M.;

RT "Direct evidence that oncogenic tyrosine kinases and cyclic AMP-dependent protein kinase have homologous ATP-binding sites.";

RL Nature 310:589-592(1984).

RN [6]

RP PHOSPHORYLATION.

RX MEDLINE=86028181; PubMed=2996780;

RA Gould K.L., Woodgett J.R., Cooper J.A., Buss J.E., Shalloway D., Hunter T.;

RT "Protein kinase C phosphorylates pp60src at a novel site.";

RL Cell 42:849-857(1985).

RN [7]

RP PHOSPHORYLATION OF TYR-415.

RX MEDLINE=82082387; PubMed=6273838;

RA Smart J.E., Oppermann H., Czernilofsky A.P., Purchio A.F., Erikson J.R., Bishop J.M.;

RT "Characterization of sites for tyrosine phosphorylation in the transforming protein of Rous sarcoma virus (pp60v-src) and its normal cellular homologue (pp60c-src).";

RL Proc. Natl. Acad. Sci. U.S.A. 78:6013-6017(1981).

RN [8]

RP PHOSPHORYLATION OF TYR-526.

RX MEDLINE=86151652; PubMed=2420005;

RA Cooper J.A., Gould K.L., Cartwright C.A., Hunter T.;

RT "Tyrosine 526 is phosphorylated in pp60c-src: implications for regulation.";

RL Science 231:1431-1434(1986).

RN [9]

RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 82-532.

RX MEDLINE=98070614; PubMed=9405157;

RA Williams J.C., Weijland A., Gonfalon S., Thompson A., Countinidge S.A., Superti-Furga G., Wierenga R.K.;

RT "The 2.35 A crystal structure of the inactivated form of chicken Src: a dynamic molecule with multiple regulatory interactions.";

RL J. Mol. Biol. 274:757-775(1997).

RN [10]

RP STRUCTURE BY NMR OF 80-139.

RX MEDLINE=93279385; PubMed=8504863;

RA Yu H., Rosen M.K., Schneider S.L.;

RT "1H and 15N assignments and secondary structure of the Src SH3 domain.";

RL FEBS Lett. 324:87-92(1993).

RN [11]

RP STRUCTURE BY NMR OF 76-139.

RX MEDLINE=95063992; PubMed=7526465;

RA Feng S., Chen J.K., Yu H., Simon J.A., Schneider S.L.;

RT "Two binding orientations for peptides to the Src SH3 domain: development of a general model for SH3-ligand interactions.";

RL Science 266:1241-1247(1994).

CC -! FUNCTION: THE FUNCTION OF PP60-C-SRC IS UNKNOWN. IT IS EXPRESSED TO HIGH LEVELS, AND WITH A HIGH DEGREE OF KINASE ACTIVITY, IN CERTAIN FULLY DIFFERENTIATED CELLS SUCH AS NEURONS, PLATELETS AND MACROPHAGES.

CC -! CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein tyrosine phosphate.

CC -! ENZYME REGULATION: BECOMES ACTIVATED WHEN ITS MAJOR TYROSINE PHOSPHORYLATION SITE IS NOT PHOSPHORYLATED. IT CAN ALSO BE ACTIVATED BY POINT MUTATIONS AS WELL AS BY TRUNCATIONS AT THE C-TERMINAL END OR BY OTHER MUTATIONS.

CC -! PTM: Phosphorylated on Tyr-526 by c-Src kinase (CSK). The phosphorylated tail interacts with the SH2 domain thereby repressing kinase activity (by similarity).

CC -! MISCELLANEOUS: POLYOMA VIRUS MIDDLE T ANTIGEN FORMS A COMPLEX WITH PP60-C-SRC.

CC -! SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC SUBFAMILY.

CC -! SIMILARITY: Contains 1 SH2 domain.

CC -! SIMILARITY: Contains 1 SH3 domain.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sdb.ch/announce/> or send an email to license@isb-sdb.ch).

CC -----

DR EMBL; V00402; CAA23696.1; -

DR EMBL; J00844; AAA70194.1; -

DR EMBL; S43604; AAD13831.1; -

DR EMBL; S43616; AAD13835.1; -

DR EMBL; S43587; AAD13830.1; -

DR EMBL; S43609; AAD13832.1; -

DR EMBL; S43619; AAD13834.1; -

DR EMBL; S43579; AAB19353.2; -

DR PIR; A00630; TVCHS.

DR PDB; 1SRJ; 31-MAY-94.

DR PDB; 1SRM; 31-MAY-94.

DR PDB; 2PTK; 24-DEC-97.

DR PDB; 1PRL; 07-FEB-97.

DR PDB; 1PRM; 07-FEB-95.

DR PDB; 1RLP; 07-FEB-95.

DR PDB; 1RLQ; 07-FEB-95.

DR PDB; 1NLO; 27-JAN-97.

DR PDB; 1NLP; 27-JAN-97.

DR PDB; 1F1W; 06-JUL-00.

DR PDB; 1F2F; 06-JUL-00.

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: July 29, 2003, 09:48:37 ; Search time 44 Seconds
(without alignments)
2973.470 Million cell updates/sec

Title: US-09-977-261-2

Sequence: 1 MAGRSLVSWRAFHGDSAE.....PASVSGQDADGSRPSRSGEP 507

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :

SPTRMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_oranelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------|
| 1 | 2544 | 95.2 | 523 | 4 | Q9NST8 |
| 2 | 2385.5 | 89.3 | 465 | 4 | Q16176 |
| 3 | 2277.5 | 85.3 | 511 | 11 | Q64103 |
| 4 | 2214.5 | 82.9 | 465 | 11 | Q9D6H7 |
| 5 | 2214.5 | 82.9 | 465 | 11 | P70223 |
| 6 | 1243.5 | 46.6 | 450 | 11 | Q8YCW1 |
| 7 | 1216.5 | 45.5 | 450 | 13 | Q73786 |
| 8 | 1004.5 | 37.6 | 485 | 5 | Q9Y1Z0 |
| 9 | 979.5 | 36.7 | 723 | 5 | Q9VCK8 |
| 10 | 976.5 | 36.6 | 467 | 5 | Q77132 |
| 11 | 751.5 | 28.1 | 509 | 11 | Q91X65 |
| 12 | 742.5 | 27.8 | 526 | 15 | Q93X80 |
| 13 | 742 | 27.8 | 502 | 13 | Q8GJ39 |
| 14 | 737.5 | 27.6 | 509 | 6 | Q95M32 |
| 15 | 736 | 27.6 | 545 | 15 | Q86362 |
| 16 | 735.5 | 27.5 | 509 | 6 | Q95KR7 |

| | | | | | | |
|----|-------|------|------|----|--------|---------------------|
| 17 | 734.5 | 27.5 | 526 | 15 | Q64994 | 064994 rous sarcom |
| 18 | 733 | 27.4 | 546 | 15 | Q86363 | 086363 rous sarcom |
| 19 | 732.5 | 27.4 | 504 | 5 | Q8WSU2 | 08WSU2 ephydalia f |
| 20 | 730.5 | 27.3 | 526 | 15 | Q07461 | 007461 rous sarcom |
| 21 | 730.5 | 27.3 | 526 | 15 | Q60567 | 060567 rous sarcom |
| 22 | 730.5 | 27.3 | 526 | 15 | Q64993 | 064993 rous sarcom |
| 23 | 730 | 27.3 | 495 | 5 | Q8WSU4 | 08WSU4 ephydalia f |
| 24 | 730 | 27.3 | 523 | 15 | Q85477 | 085477 rous sarcom |
| 25 | 729 | 27.3 | 535 | 15 | Q92957 | 092957 rous sarcom |
| 26 | 728.5 | 27.3 | 587 | 15 | Q64817 | 064817 avian sarco. |
| 27 | 724 | 27.1 | 1620 | 5 | Q9VY86 | Q9VY86 drosophila |
| 28 | 723.5 | 27.1 | 526 | 15 | Q92806 | 092806 rous sarcom |
| 29 | 716.5 | 26.8 | 502 | 13 | Q9DDK6 | 09DDK6 salmo salar |
| 30 | 715 | 26.8 | 542 | 11 | Q9J10 | 09J10 rattus norv |
| 31 | 711 | 26.6 | 488 | 13 | Q13064 | 013064 xenopus lae |
| 32 | 710 | 26.6 | 541 | 11 | Q99PW1 | 099PW1 rattus norv |
| 33 | 706 | 26.4 | 499 | 11 | Q8K2M8 | 08K2M8 mus musculu |
| 34 | 706 | 26.4 | 541 | 11 | Q8CBP1 | 08CBP1 mus musculu |
| 35 | 703 | 26.3 | 491 | 11 | Q8CE10 | 08CE10 mus musculu |
| 36 | 702 | 26.3 | 541 | 11 | Q8C762 | 08C762 mus musculu |
| 37 | 698 | 26.1 | 525 | 13 | Q8AWF1 | 08AWF1 brachydanio |
| 38 | 698 | 26.1 | 537 | 11 | Q62844 | 062844 rattus norv |
| 39 | 697 | 26.1 | 812 | 15 | Q85466 | 085466 y73 sarcoma |
| 40 | 697 | 26.1 | 823 | 6 | Q9TTY2 | 09TTY2 canis fami |
| 41 | 695 | 26.0 | 505 | 4 | Q961N1 | 0961N1 homo sapien |
| 42 | 694 | 26.0 | 527 | 13 | Q91952 | 091952 xiphophorus |
| 43 | 693.5 | 26.0 | 470 | 5 | Q8WSU3 | 08WSU3 ephydalia f |
| 44 | 691.5 | 25.9 | 466 | 13 | Q93411 | 093411 xenopus lae |
| 45 | 689.5 | 25.8 | 527 | 5 | Q9Y121 | 09Y121 ephydalia f |

ALIGNMENTS

RESULT 1
ID Q9NST8 PRELIMINARY; PRT; 523 AA.
AC Q9NST8;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein (Fragment).
GN DKFZP34N1212.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Duesterhoeft A., Lauber J., Mewes H.W., Weil B., Wiemann S.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR EMBL; AL137754; CAB70906.1; -;
DR HSSP; P11362; IFGK.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR000980; SH2.
DR InterPro: IPR001452; SH3.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam; PF00069; pkinase.1.
DR Pfam; PF00017; SH2.1.
DR Pfam; PF00018; SH3.1.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00109; TYRKINASE.
DR PRODOM; PD000001; Prot_kinase.1.
DR PRODOM; PD000093; SH2.1.
DR SMART; SM00252; SH2.1.
DR SMART; SM00326; SH3.1.
DR SMART; SM00219; TYKCa.1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP.1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM.1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR.1.
DR PROSITE; PS50001; SH2.1.

DR PROSITE; PS50002; SH3; 1.
 KW Hypothetical protein; Kinase; SH3 domain; Transferase;
 FT Tyrosine-protein kinase.
 SQ SEQUENCE 523 AA; 57776 MW; C246280FD7890AFE CRC64;
 NON_TER 1 1
 Query Match 95.2%; Score 2544; DB 4; Length 523;
 Best Local Similarity 96.4%; Pred. No. 3.7e-198;
 Matches 488; Conservative 1; Mismatches 5; Indels 12; Gaps 1;

QY 2 AGRGSLVSMRAHGCOSAEELPRVSPRFLRAHMPPVSAHMPRRAPGTCCTCKEHR 61
 DB 30 AGRG-----SGAPRDSVSPFLRAHMPPVSAHMPRRAPGTCCTCKEHR 77
 QY 62 PRGELAFRRKGDVVTILEACENKSWYRVKHTSGOGLLAAGALRREALSADPKSLMP 121
 DB 78 PRGELAFRRKGDVVTILEACENKSWYRVKHTSGOGLLAAGALRREALSADPKSLMP 137
 QY 122 WPHGKISGOEAVQOLPPEDGLFLVRESARHPEDVLCVSGRDVTHYVLRHGHLLTD 181
 DB 138 WPHGKISGOEAVQOLPPEDGLFLVRESARHPEDVLCVSGRDVTHYVLRHGHLLTD 197
 QY 182 EAVFECNLMDVNEHYSKDKGALCTKLYPRKRKHGTSAEELARAGWLNLQHLTGAQI 241
 DB 198 EAVFECNLMDVNEHYSKDKGALCTKLYPRKRKHGTSAEELARAGWLNLQHLTGAQI 257
 QY 242 GGEFGAVLQGEYLGOKVAVKNKCDVTAQAFLEDAVMTKQHEMLVRLGLVILHOGLY 301
 DB 258 GGEFGAVLQGEYLGOKVAVKNKCDVTAQAFLEDAVMTKQHEMLVRLGLVILHOGLY 317
 QY 302 IYMEHVSKNLVNFLTFRALVNTAQLQFSLHVAEGMEYLESKLVHRLAARILVS 361
 DB 318 IYMEHVSKNLVNFLTFRALVNTAQLQFSLHVAEGMEYLESKLVHRLAARILVS 377
 QY 362 EDLVAVSPFGIAKAKERKGLDSSRLPVKMTAPALKHGFTSKSDVMSGVLMEVSYG 421
 DB 378 EDLVAVSPFGIAKAKERKGLDSSRLPVKMTAPALKHGFTSKSDVMSGVLMEVSYG 437
 QY 422 RAPYPRMSLKEVSEAVEKGRMEPPGCGPVHVLMSGCWEAEAPARRPFRLAEKLARE 481
 DB 438 RAPYPRMSLKEVSEAVEKGRMEPPGCGPVHVLMSGCWEAEAPARRPFRLAEKLARE 497
 QY 482 LRSAGAPASVSGODADGSTSPRSQEP 507
 DB 498 LRSAGAPASVSGODADGSTSPRSQEP 523

RESULT 2
 016176 PRELIMINARY; PRT; 465 AA.
 AC 016176;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, last sequence update)
 DE 01-MAR-2003 (Tremblrel. 23, last annotation update)
 GN LSK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-94268844; PubMed-7516063;
 RA McVicar D.W., Lal B.R., Lloyd A., Kawamura M., Chen Y.Q.; Zhang X.,
 RA Staples J.E., Ortaldo J.R., O'Shea J.J.;
 RT "Molecular cloning of lsk, a carboxyl-terminal src kinase (csk)
 RT related gene, expressed in leukocytes.";
 RT Oncogene 9:2037-2044(1994).
 CC -I- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 DR EMBL; S71659; AAB30995.1; -;
 DR HSSP; P11362; IFGR.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR000980; SH2.

DR InterPro; IPR001452; SH3.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00006; pkinase; 1.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; TYRKC; 1.
 DR PROSITE; PS50019; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW ATP-binding; Kinase; SH3 domain; Transferase; Tyrosine-protein kinase.
 SQ SEQUENCE 465 AA; 51908 MW; 504B4E8078320C35 CRC64;
 NON_TER 1 1
 Query Match 89.3%; Score 2385.5; DB 4; Length 465;
 Best Local Similarity 98.1%; Pred. No. 2.4e-185;
 Matches 457; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

QY 42 MPTRRAPGTCCTCKEHRPRKPGELAFRRKGDVVTILEACENKSWYRVKHTSGOGLLA 101
 DB 1 MPTRRAPGTCCTCKEHRPRKPGELAFRRKGDVVTILEACENKSWYRVKHTSGOGLLA 60
 QY 102 AGALRREALSADPKSLMPWFHGRKISGOEAVQOLPPEDGLFLVRESARHPEDVLCVS 161
 DB 61 AGALRREALSADPKSLMPWFHGRKISGOEAVQOLPPEDGLFLVRESARHPEDVLCVS 120
 QY 162 FGRDVIHYVLRHGHLLTDEAVFECNLMDVNEHYSKDKGALCTKLYPRKRKHGTSAE 221
 DB 121 FGRDVIHYVLRHGHLLTDEAVFECNLMDVNEHYSKDKGALCTKLYPRKRKHGTSAE 180
 QY 222 ELARAGWLNLQHLTGAQIGGEFGAVLQGEYLGOKVAVKNKCDVTAQAFLEDAVMT 281
 DB 181 ELARAGWLNLQHLTGAQIGGEFGAVLQGEYLGOK -CVNKKCDVTAQAFLEDAVMT 239
 QY 282 KQHEMLVRLGLVILHOGIYIYMEHVSKNLVNFLTFRALVNTAQLQFSLHVAEGME 341
 DB 240 KQHEMLVRLGLVILHOGIYIYMEHVSKNLVNFLTFRALVNTAQLQFSLHVAEGME 299
 QY 342 YLESKLVHRLAARILVSEDLVAKVSPFGIAKAKERKGLDSSRLPVKMTAPALKHGFT 401
 DB 300 YLESKLVHRLAARILVSEDLVAKVSPFGIAKAKERKGLDSSRLPVKMTAPALKHGFT 359
 QY 402 TSKSDVMSGVLMEVSYGRAPYPRMSLKEVSEAVEKGRMEPPGCGPVHVLMSGCW 461
 DB 360 TSKSDVMSGVLMEVSYGRAPYPRMSLKEVSEAVEKGRMEPPGCGPVHVLMSGCW 419
 QY 462 EAEPPARRPFRLAEKLARELSAGAPASVSGODADGSTSPRSQEP 507
 DB 420 EAEPPARRPFRLAEKLARELSAGAPASVSGODADGSTSPRSQEP 465

RESULT 3
 064103 PRELIMINARY; PRT; 511 AA.
 AC 064103;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, last sequence update)
 DE 01-MAR-2003 (Tremblrel. 23, last annotation update)
 GN VNK.
 OS Mus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10095;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-95178994; PubMed-7874011;
 RA Ershler M.A., Krivtsov A.V., Krotkova A.V., Beliavskii A.V.,
 RA Visser J.V.;
 RT "Vnk-a new gene for nonreceptor protein-tyrosine kinase, expressed

| | | | | |
|----|-----|--|-----|-----|
| QY | 222 | ELARAGMLINTLOHLLTGAOIGSEGGAVLYOGSYLGOKYAVNNICODYTAQAFIDETA | VMT | 281 |
| | | | | |
| | 180 | ELKACAGMLDLOHLLTGAOIGSEGGAVLYOGSYLGOKYAVNNICODYTAQAFIDETA | VMT | 239 |
| | | | | |
| QY | 282 | KMOHENIVLLGLVILHQGLYIVMEVHSKGNLWPLRTGRALVYTAOLLOFSLHVAEGME | | 341 |
| | | | | |
| | 240 | KLOHRNIVLLGLVILHQGLYIVMEVHSKGNLWPLRTGRALVYTAOLLOFSLHVAEGME | | 299 |
| | | | | |
| QY | 342 | YLESKTLVHRDLAARNILVSEDLVAKVNSPFGIAKERGLDSSRLPVYKWTAPALAKRGKF | | 401 |
| | | | | |
| | 300 | YLESKTLVHRDLAARNILVSEDLVAKVNSPFGIAKERGLDSSRLPVYKWTAPALAKRGKF | | 359 |
| | | | | |
| QY | 402 | TSKSDVWSGCVLLMEVFSYGRAPYPRMSLKEVSEAVEYKGYRMEPEPGCPGVHVLMSGCN | | 461 |
| | | | | |
| | 360 | SKSDVWSGCVLLMEVFSYGRAPYPRMSLKEVSEAVEYKGYRMEPEPGCPGVHVLMSGCN | | 419 |
| | | | | |
| QY | 462 | EAPPARPPPRKLAELKLAELASAPASVSGQDDAGSTSPRSQEP | | 507 |
| | | | | |
| | 420 | EAPPARPPPRKLAELKLAELASAPASVSGQDDAGSTSPRSQEP | | 465 |
| | | | | |

RESULT 5

| ID | PROT223 | PRELIMINARY; | PRT; | 465 AA. |
|----|--|--------------|------|---------|
| AC | P70223; | | | |
| DT | 01-FEB-1997 (TrEMBLrel. 02, Created) | | | |
| DT | 01-FEB-1997 (TrEMBLrel. 02, Last sequence update) | | | |
| DT | 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) | | | |
| DE | HYL tyrosine kinase. | | | |
| GN | MAPK OR HYLK. | | | |
| OS | Mus musculus (Mouse). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Euteleota; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | |
| OX | NCBI_TaxID=10090; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | SPRAIN-CBA X C57BL/6; TISSUE=Embryonic stem; | | | |
| RX | MEDLINE=96280730; Pubmed=8694808; | | | |
| RA | Hanaguchi I., Yamaguchi N., Suda J., Iwama A., Hirao A., Hashiyama M., | | | |
| RA | Atsava S.I., Suda T.; | | | |
| RT | "Analysis of csk homologous kinase (CHK/HYL) in hematopoiesis by | | | |
| RT | utilizing gene knockout mice.;" | | | |
| RL | Biochem. Biophys. Res. Commun. 224:172-179(1996). | | | |
| CC | 1- SIMILARITY: CONTAINS 1 SH3 DOMAIN. | | | |
| DR | EMBL: X83972; CA58806.1; . | | | |
| DR | HSSP: P11362; ICGK | | | |
| DR | MED: MG1:99259; Matk. | | | |
| DR | InterPro: IPR000719; Prot_Kinase. | | | |
| DR | InterPro: IPR000980; SH2. | | | |
| DR | InterPro: IPR001452; SH3. | | | |
| DR | InterPro: IPR001245; Tyr_Pkinase. | | | |
| DR | Pfam: PF00069; pkinase.1. | | | |
| DR | Pfam: PF00017; SH2.1. | | | |
| DR | Pfam: PF00018; SH3.1. | | | |
| DR | PRINTS: PR00401; SH2DOMAIN. | | | |
| DR | PRINTS: PR00109; TYRKINASE. | | | |
| DR | ProDom: PD000001; Prot_kinase; 1. | | | |
| DR | ProDom: PD000093; SH2.1. | | | |
| DR | SMART: SM00252; SH2.1. | | | |
| DR | SMART: SM00326; SH3.1. | | | |
| DR | SMART: SM00219; TYRKc.1. | | | |
| DR | PROSITE: PS00107; PROTEIN_KINASE_AKP; 1. | | | |
| DR | PROSITE: PS50011; PROTEIN_KINASE_DOM; 1. | | | |
| DR | PROSITE: PS00109; PROTEIN_KINASE_TYR; 1. | | | |
| DR | PROSITE: PS50001; SH2.1. | | | |
| DR | PROSITE: PS50002; SH3.1. | | | |
| DR | AP-Blinding; Kinase; SH3 domain; Transferase; Tyrosine-protein kinase | | | |
| Q0 | SEQUENCE 465 AA; 51571 MW; 24C2DBA71A08A3E9 CRC64; | | | |

| | | | | |
|-----------------------|------------------|---------------------|-----------|-------------|
| Query Match | 82.9%; | Score 2214.5; | DB 11; | Length 465; |
| Best Local Similarity | 89.5%; | Pred. No. 1.9e-171; | | |
| Matches 417; | Conservative 24; | Mismatches 24; | Indels 1; | Gaps 1; |

| | | | |
|----|-----|---|-----|
| Qy | 42 | MpRRRABPGCCTCKEHNRPRKRGELARRKGVYIILACENKSMYRKXHHHTSQEBLLA | 101 |
| Db | 1 | MpI-KNAPGTCCTCKENSRPKRGELARRKGVYIILACEDKSMYRKXHHHTSQEBLLA | 59 |
| Qy | 102 | AGALRRREALSADPKSLMPMFHGRKISGGEAAVOQLQDPEDDLFLVRESARHPGDYLCVS | 161 |
| Db | 60 | AAALRRREALSTDPKSLMPMFHGRKISGGEALQQLPDEDLFLVRESARHPGDYLCVS | 119 |
| Qy | 162 | FGSDVYHYRVLHRHDGLTIDEAVFPCNLMDWYEHNSKRGALCTKRLVRRPKKHHTKSAEE | 221 |
| Db | 120 | FGSDVYHYRVLHRHDGLTIDEAVFCNCLMDWYEHNTKRGALCTKRLVRRPKRQAKSAEE | 179 |
| Qy | 222 | ELRAGMLNLQHLTLTGAAQIGSGEGFAGVLOGEYLOQKAAVANNICDVTAAQAFLEDTAVMT | 281 |
| Db | 180 | ELAKAGMLDLQHLTLTGAAQIGSGEGFAGVLOGEYLSQKAAVANNICDVTAAQAFLEDTAVMT | 239 |
| Qy | 282 | KMOHENVLRLGLVILHQGLTYMEHVHNSKGNLVNPLRTGRALVNTAQLLOSLHVAEGME | 341 |
| Db | 240 | KLOHRMLVRLGLVILHHGLTYMEHVHNSKGNLVNPLRTGRALVNTSOLLOFALHVAEGME | 299 |
| Qy | 342 | YLESKKLVRDLAARHILVSEDLVAKVSPGLAKERGLDSSRPLPVKMTAPALAKHGRF | 401 |
| Db | 300 | YLESKKLVRHDLAARHILVSEDLVAKVSPGLAKERGLDSSRPLPVKMTAPALAKHGRF | 358 |
| Qy | 402 | TSKSDWMSFGVLLMEFVTSYGRAPYPKMSLKEVSEAVEKGYRMEPEPGCPGVHVLMSGCW | 461 |
| Db | 360 | SKSDWMSFGVLLMEFVTSYGRAPYPKMSLKEVSEAVEKGYRMEPEPGCPGVHVLMSGCW | 419 |
| Qy | 462 | EAEPARRRPPRKIAEKLABELRSAGAPASVSGQDADGSTSPRSQEP | 507 |
| Db | 420 | EAEPARRRPPRKIVLEKLGRELRSVSGPAGQGEAEKSGAPRRSDP | 465 |

RESULT 6

| ID | ORGANISM | PRELIMINARY | PR | AA |
|----|---|------------------------|----|----|
| AC | 08VCM1 | | | |
| DT | 01-MAR-2002 (TREMBLrel. 20) | Created | | |
| DT | 01-MAR-2002 (TREMBLrel. 20) | Last sequence update | | |
| DT | 01-MAR-2003 (TREMBLrel. 23) | Last annotation update | | |
| DE | C-src tyrosine kinase. | | | |
| GN | CSK. | | | |
| OS | Mus musculus (Mouse). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus | | | |
| OX | NCBI_TaxId=10090; | | | |
| RN | [1] | | | |
| RC | SEQUENCE FROM N.A. | | | |
| RP | TISSUE-Colon; | | | |
| RA | Strasberg R.; | | | |
| RL | Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases. | | | |
| CC | -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN. | | | |
| DR | EMBL: BC018394; AAH18394.1; - | | | |
| DR | MGD; MGI:88537; CSK. | | | |
| DR | InterPro: IPR000719; Prot_kinase. | | | |
| DR | InterPro: IPR000980; SH2. | | | |
| DR | InterPro: IPR001452; SH3. | | | |
| DR | InterPro: IPR001245; Tyr_kinase. | | | |
| DR | Pfam: PF000069; pkinase.1. | | | |
| DR | Pfam: PF00017; SH2.1. | | | |
| DR | Pfam: PF00018; SH3.1. | | | |
| DR | PRINTS: PR00401; SH2DOMAIN. | | | |
| DR | PRINTS: PR00109; TYRKINASE. | | | |
| DR | ProDom: PD000001; Prot_kinase.1. | | | |
| DR | ProDom: PD000093; SH2.1. | | | |
| DR | ProDom: PD000066; SH3.1. | | | |
| DR | SMART: SM00252; SH2.1. | | | |
| DR | SMART: SM00326; SH3.1. | | | |
| DR | SMART: SM00219; Tyrc.1. | | | |
| DR | PROSITE: PS00107; PROTEIN_KINASE_ATP.1. | | | |
| DR | PROSITE: PS50011; PROTEIN_KINASE_DOM.1. | | | |
| DR | PROSITE: PS00109; PROTEIN_KINASE_TYR.1. | | | |

DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW ATP-binding; Kinase; SH3 domain; Transferase; Tyrosine-protein kinase.
 SO SEQUENCE 450 AA; 50716 MW; E8D3EC9357B86277 CRC64;

Query Match 46.6%; Score 1243.5; DB 11; Length 450;
 Best Local Similarity 54.1%; Pred. No. 1.5e-92;

Matches 235; Conservative 83; Mismatches 115; Indels 3; Gaps 2;

QY 47 WAPGTCITKCEHTPRPGELAFKRGDVVTILEACENKSWYRKVNHHTSGDEGLAAGLR 106
 DB 8 WPGTECIAKYNFHGTAEDLPFCCKGDVLTIVAVTKDPNMYKAKNKV-GREGIIPANYQ 66
 QY 107 EREALSDPKLSLMPWFHKGITSGOEAQOOLPPEDGFLVRESARHPGDVLCVSPGRDY 166
 DB 67 KREGVAKGKTLSTLMPWFHKGITRQAEKRLIPETGLFVRESINPDGYTLVCSCGKY 126
 QY 167 IHVRLRGHLTIDEAVFPCNLMDVNEHYSKDKGALCTKLVPRKRGHTKSABEELARA 226
 DB 127 EHYRIMYHASKLSIDEVEYFENLMQVLEHYTTDADGLCTRLIKPKVEGVAAQDEFYRS 186
 QY 227 GWLNLQHLTGLGQIGEGGAVLQGYLGOKYAVKIKCDVTAQAFLDETAVNTKQHE 286
 DB 187 GWALNKKELKLTQIGEGGAVLQGYLGOKYAVKIKCDVTAQAFLDETAVNTKQHE 246
 QY 287 NLVRLGLVILH--GLYIVNEHYSKGLVNFRTGRGALVNTAQLQFSLHVAEGMYLE 344
 DB 247 NLVQLGLVILH--GLYIVNEHYSKGLVNFRTGRGALVNTAQLQFSLHVAEGMYLE 306
 QY 345 SKRLVHRDLAARNILVSEDLVAKVSDPGLAKAEKRGDSSRLPYKMTAPEALKHGFSTK 404
 DB 307 GNNFVHRDLAARNILVSEDLVAKVSDPGLAKAEKRGDSSRLPYKMTAPEALKHGFSTK 366
 QY 405 SDVWSFGVLLMEVFSYGRADYPKMSLKEVSEAVEKGYRMEPPBECGPVHYLMSSCWEAE 464
 DB 367 SDVWSFGVLLMEVFSYGRADYPKMSLKEVSEAVEKGYRMEPPBECGPVHYLMSSCWEAE 426
 QY 465 PARPPPRKLAELK 478
 DB 427 PARPPPRKLAELK 440

RESULT 7
 073786 PRELIMINARY; PRT; 450 AA.
 AC 073786;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE C-Src kinase.
 GN CSK.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_Taxid=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Murphy S.M., Morgan D.O.;
 RT "Identification of Xenopus c-Src Kinase (CSK) using a genetic screen
 for suppressors of c-Src activity in the budding yeast, *Saccharomyces
 cerevisiae*.";
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 DR EMBL; AF052430; AAC05835.1; -;
 DR HSSP; P41240; 1CSK.
 DR InterPro: IPR000719; ProL_Kinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001245; Tyr_Kinase.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.

DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR PRODOM; PD000001; ProL_Kinase; 1.
 DR PRODOM; PD000093; SH2; 1.
 DR PRODOM; PD000066; SH3; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; TYRK; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW ATP-binding; Kinase; SH3 domain; Transferase; Tyrosine-protein kinase.
 SO SEQUENCE 450 AA; 50807 MW; F02FE0357679BA53 CRC64;

Query Match 45.5%; Score 1216.5; DB 13; Length 450;
 Best Local Similarity 52.7%; Pred. No. 2.4e-90;
 Matches 233; Conservative 83; Mismatches 119; Indels 7; Gaps 3;

QY 47 WAPGTCITKCEHTPRPGELAFKRGDVVTILEACENKSWYRKVNHHTSGDEGLAAGLR 106
 DB 8 WQAGIECIANYDFQGAEDLDPSKGEVLTIVAVTKDPNMYKAKNKV-GRVGFIPANYQ 66
 QY 107 EREALSDPKLSLMPWFHKGITSGOEAQOOLPPEDGFLVRESARHPGDVLCVSPGRDY 166
 DB 67 KREGVAKGKTLSTLMPWFHKGITRQAEKRLIPETGLFVRESINPDGYTLVCSCGKY 126
 QY 167 IHVRLRGHLTIDEAVFPCNLMDVNEHYSKDKGALCTKLVPRKRGHTKSABEELARA 226
 DB 127 EHYRIIYSSGSLSIDEVEYFENLMQVLEHYTTDADGLCTNLIKRLMEGVTAADDEFYRS 186
 QY 227 GWLNLQHLTGLGQIGEGGAVLQGYLGOKYAVKIKCDVTAQAFLDETAVNTKQHE 286
 DB 187 GWALNKKELKLTQIGEGGAVLQGYLGOKYAVKIKCDVTAQAFLDETAVNTKQHE 246
 QY 287 NLVRLGLVILH--OGLYIVNEHYSKGLVNFRTGRGALVNTAQLQFSLHVAEGMYLE 344
 DB 247 NLVQLGLVILH--OGLYIVNEHYSKGLVNFRTGRGALVNTAQLQFSLHVAEGMYLE 306
 QY 345 SKRLVHRDLAARNILVSEDLVAKVSDPGLAKAEKRGDSSRLPYKMTAPEALKHGFSTK 404
 DB 307 SNNFVHRDLAARNILVSEDLVAKVSDPGLAKAEKRGDSSRLPYKMTAPEALKHGFSTK 366
 QY 405 SDVWSFGVLLMEVFSYGRADYPKMSLKEVSEAVEKGYRMEPPBECGPVHYLMSSCWEAE 464
 DB 367 SDVWSFGVLLMEVFSYGRADYPKMSLKEVSEAVEKGYRMEPPBECGPVHYLMSSCWEAE 426
 QY 465 PARPPPRKLAELK----AREL 482
 DB 427 PKORPTFRLREOLEHIAKEL 448

RESULT 8
 09Y120 PRELIMINARY; PRT; 485 AA.
 AC 09Y120;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Protein tyrosine kinase.
 GN EPPTK1.
 OS Ephydatia fluviatilis.
 OC Eukaryota; Metazoa; Porifera; Demospongiae; Ceractinomorpha;
 OC Haplosclerida; Spongillidae; Ephydatia.
 OX NCBI_Taxid=31330;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-99246375; PubMed-10229566;
 RA Suga H., Koyanagi M., Hoshiyama D., Ono K., Iwabe N., Kuma K.,
 Miyata T.;
 RT "Extensive gene duplication in the early evolution of animals before

RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RA Mista S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celinker S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Krommiller B., Marshall B., Milburn G., Richter J., Russo S.,
RA Seale S.M.J., Smith E., Shu S., Smutnick F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.,
RT Annotation of Drosophila melanogaster genome.
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
[4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celinker S.E., Gibbs R.A., Rubin G.M., Venter C.J.,
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
[5]
RP SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (SEP-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL: AE003692; AAF54668.2; -
DR HSSP: P11362; ICSK. CG17309.
DR FlyBase: FBgn0037925; CG17309.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR000980; SH2.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF00017; SH2; 1.
DR PRINTS: PR00401; SH2DOMAIN.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Prot_kinase; 1.
DR ProDom: PD000093; SH2; 1.
DR SMART: SM00252; SH2; 1.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00219; TyKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS50001; SH2; 1.
DR ATP-binding; Transferase.
KW SEQUENCE 723 AA; 78047 MW; 98C596A6A450AF6B CRC64; .
Query Match 36.7%; Score 979.5; DB 5; Length 723;
Best Local Similarity 48.8%; Pred. No. 9e-71;
Matches 191; Conservative 72; Mismatches 123; Indels 5; Gaps 3;
QY 93 TSGEGLLAAGALBEREALS-ADPKLSLMPFHGKISGQEAVALQPPEDGLFTVRESAR 151
DB 325 TAMNHASISPTALAPQOGRSCEVKLNAMPWFHGSITRDEAHLLOPPEDGLFTVRESTN 384
QY 152 HPGDYVLCVSGRQVYIHRYLHROGHLTIDEAVFCNLMDEVHYSKKGALCTKLVPK 211
DB 385 FPGDYVLCVSGRQVYIHRYLHROGHLTIDEAVFCNLMDEVHYSKKGALCTKLVPK 444
QY 212 RKHGTRK---AEELARAGWMLNLQHLTLGAQIGEGFGAVLQGYLQKAVVNIKCDV 268
DB 445 PKLGKQRCINSKQPVFKGWYIPRAEQLDRESIGKEGDDVMLGILNREKAYAVMKLKEG 504
QY 269 TQAQFLDETAVTGMQHEINLVRLGVIL-HQGLYVMEHVSKGMLNVLRTGRALVNTA 327
DB 505 AVQKFLAASVMTLEHNLVKFGLVFTSKHLYVTEYMSKGLVDYLRSGRQHITKK 564
QY 328 QLLQSLVHAEGMEYLESKLYVHRLDARNLVSDVLAQVSDGLAAEKKGDSRLP 387
DB 565 DQILFADVTAGMEYLESKLYVHRLDARNLVSDVLAQVSDGLAAEKKGDSRLP 624
QY 388 VKMTAPEALHKGKFTSKDVSFGVILMEVFSGAPYKMSLKEVSAVEKGYRMEPPE 447
DB 625 IKMTAPEALHKGKFTSKDVSFGVILMEVFSGAPYKMSLKEVSAVEKGYRMEPPE 684
QY 448 GCPGVHVLWSSCWEAEPRRPPFKLAETL 478

DB 685 GCPPEYEMRQAMDLNPAKRPTFAELVKVL 715
RESULT 10
ID 077132 PRELIMINARY; PRT; 467 AA.
AC 077132; Q25195;
DT 01-NOV-1998 (TREMBLrel. 08. Created)
DT 01-NOV-1998 (TREMBLrel. 08. Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23. Last annotation update)
DE Non-receptor protein-tyrosine kinase CSK.
GN CSK.
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroids; Anthomedusae;
OC Hydidae; Hydra.
OX NCBI_TaxID=6087;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-UCI;
RX MEDLINE-20408254; PubMed-10951585;
RA Miller M.A., Malik I.A., Shenk M.A., Steele R.E.,
RT "The Src/Csk regulatory circuit arose early in metazoan evolution."
RN Oncogene 19:3925-3930(2000).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN-UCI;
RA Steele R.E.;
RL Submitted (SEP-1998) to the EMBL/Genbank/DBJ databases.
CC -1 SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR EMBL: AF067775; AAC35011.1; -
DR HSSP: P41240; ICSK.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR000980; SH2.
DR InterPro: IPR001452; SH3.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00018; SH3; 1.
DR PRINTS: PR00401; SH2DOMAIN.
DR PRINTS: PR00452; SH3DOMAIN.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Prot_kinase; 1.
DR ProDom: PD000093; SH2; 1.
DR ProDom: PD000066; SH3; 1.
DR SMART: SM00252; SH2; 1.
DR SMART: SM00326; SH3; 1.
DR SMART: SM00219; TyKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS50002; SH3; 1.
DR PROSITE: PS50001; SH2; 1.
DR ATP-binding; Kinase; Receptor; SH3 domain; Transferase;
KW Tyrosine-protein kinase.
KW SEQUENCE 467 AA; 53349 MW; 64A55016B855F2F CRC64;
Query Match 36.6%; Score 976.5; DB 5; Length 467;
Best Local Similarity 43.4%; Pred. No. 8.2e-71;
Matches 196; Conservative 93; Mismatches 148; Indels 15; Gaps 8;
QY 37 PVASAMPTRRPAAPGQCITKCEHTPRKGEIAFRKGVAVTTLIACENSKYRVKHNHSGQ 96
DB 12 PMSGN-SKKNPNGNECARDFGNSKQDLPRFKGDIILLOSTYRDNRWVNAKKVSDGR 70
QY 97 EGLAAGALRREALSDAPKLSLMWFHKGISGQEAVALQPPEDGLFTVRESARHPDY 156
DB 71 TGLIPINIVQORRAL---HLHEMPWFPGKITREKAEELTPREVGLFTVRESTNFPEDY 126
QY 157 VLVCY---SFGDVIHYRYLH-RDGHLLTIDEAVFCNLMDEVHYSKKGALCTKLVPK-- 210
DB 127 TLVCVSPQNNKKVHEHYRISTSDNOVYVDEEAFPTLTLELTKHREKDDGCTMLKKPKL 186
QY 211 KRKHGTRSA---EEELARAGWMLNLQHLTLGAQIGEGFGAVLQGYLQKAVVNIKCD- 267

[illegible]

DR Pfam: PF00018; SH3; 1.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR ProDom: PD000093; SH2; 1.
 DR ProDom: PD000066; SH3; 1.
 DR SMART: SM00252; SH2; 1.
 DR SMART: SM00326; SH3; 1.
 DR SMART: SM00219; TYRKC; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 DR ATP-binding: Kinase; SH3 domain; Transferase; Tyrosine-protein kinase.
 SO SEQUENCE 509 AA; 57946 MW; F1BFE5C237C8BD7E CRC64;

Query Match 27.6%; Score 737.5; DB 6; Length 509;
 Best Local Similarity 37.4%; Pred. No. 2,5e-51;
 Matches 160; Conservative 87; Mismatches 156; Indels 25; Gaps 9;

QY 65 GELAFKGVDTLLEACENKSWYKHHHTSGOGLLAAGALREALSDPKSLMPFH 124
 DB 78 GDGFCKGEQLRLE--QSGEMWKAOSLTGGDFIFPNFVAKANSELEP-----PWF 129
 QY 125 GKISGQEAVALQPPED--GLFLVRESARHPGDYVLCV-----SFGRDYIHYRVLRD-G 176
 DB 130 KNLSDARERQLLAPGNTGHSFLIRESESTAGSFLSVNDEPDQNGEYVKKYIRMLDG 189
 QY 177 HLITDAVFFCNLMDEVHYSKDKGALCTKLVPRKHKHGTSAEELARAGCLINQHLT 236
 DB 190 GFYISPRITFPFGLHLYRHTNASDGLCTRLSRPC---TQKQPKWMEDEWEPRETLK 246
 QY 237 LGAOIEGEGGAVLOGEYLGO--KVAVKNIK-CDVTAQAFLEDEFAVNTKKOHEMLVLLGY 294
 DB 247 LVERLGAQGPGEVEMWYIYNGHTVAVKSLQSGMSMDALAEANLKKOLQHLVLLYAV 306
 QY 295 ILHGLIYVMEHVSKNLVNPLNTRGRLVNTAQLLOFSLHVAEGMEYLESKRLVHRDLA 354
 DB 307 VQEPETIITEYEMENGLVDFLKAIPSGIKITLNKLDMAAQIAEGMAFIEERNYIHRDLR 366
 QY 355 ARHIIYSEDLVAKVSPGLAKA----ERKGLDSSRLPVWTAPALKHGFTSKSVWSF 410
 DB 367 AANILVSDTLSCIAIOFGLARLLEDEYTAAREGAKPIKWTAEALNIGFTITKSDVWSF 426
 QY 411 GVLLMEFVSYGRAPYKMSLKEVSEAVENKGYRMEPECCPGPVHVLSSCMEAPARPP 470
 DB 427 GILLETIVHGRIPYGMNTPEYIQLNLENGYRMYVRDNCPEELIYQLMLCMKREPRDPT 486
 QY 471 FRKLAERL 478
 DB 487 FDLRSVL 494

RESULT 15

Q86362 PRELIMINARY; PRT; 545 AA.

AC Q86362; 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE PP62V.
 GN SRC1M.
 OS Rous sarcoma virus.
 OC Viruses; Retroviruses; Retroviridae; Alpharetrovirus.
 OX NCBI_TaxID:11886;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=66182936; PubMed=8607264;
 RA Tatosyan A., Yatsula B., Shitman M., Molnova E., Kaverina I.,
 Musatkina E., Leskov K., Mizenina O., Zueva E., Calothy G.,
 Dezelee P.;

RT "Two new isoforms of v-src oncogene isolated from low and high
 metastatic RSV-transformed hamster cells."
 RL Virology 216:347-356(1996).
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 DR EMBL: X84074; CAA58881.1; -.
 DR HSSP: P00524; 1SPR.

DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR ProDom: PD000093; SH2; 1.
 DR ProDom: PD000066; SH3; 1.
 DR SMART: SM00252; SH2; 1.
 DR SMART: SM00326; SH3; 1.
 DR SMART: SM00219; TYRKC; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 DR ATP-binding: Kinase; SH3 domain; Transferase; Tyrosine-protein kinase.
 SO SEQUENCE 545 AA; 61037 MW; 4C4E34BC75266913 CRC64;

Query Match 27.6%; Score 736; DB 15; Length 545;
 Best Local Similarity 35.6%; Pred. No. 3.7e-51;
 Matches 187; Conservative 82; Mismatches 181; Indels 76; Gaps 16;

QY 14 HCDGSAEELPR-----VSPFLRAWHPP-----PVSAMPTRRMAPGT----- 51
 DB 26 HGFPAQSPTPKNTAPLTAAPRSSR--RPAASORRAAPRTHTTPRSF--GIVANPEKLF 81
 QY 52 -----QCTIKCEHTRPKPG-----ELAFKKGVDVTLLEACENKSWYR 88
 DB 82 GFNTSDVTSPOARATLGAVTTFVALYDESMWLETDLSPFKKGERLQVNTTEG-NMWL 140
 QY 89 VKNHHTSGOGLLAAGALREALSDPKSLMPWHGKTSISGQEAVALQPPED--GLFLV 146
 DB 141 AHSVTTGQGYIPSNVAPSDSIQAE-----EMWFGKITRRESGRLNLPENPGTFV 194
 QY 147 RESARHPGYVLCVS-----FGRDYIHYRVLRD-GHLITDAVFFCNLMDEVHYSKDK 200
 DB 195 RESSETTKGAYCISVSDPFDNAKGLNKHYYIRKLDGSGFYITSRQPSLQQLVAYYSKHA 254
 QY 201 GAICTKL--VRPKRHGKTSAEELARAGCLINQHLITGAOIGEGEGAVLOGEYLQ-Q 257
 DB 255 DGLCHRLTNVCPSTSKPQTGG---LAKDAWEIPRESIRLEVLKGGCGFEGVMGTWNGTT 310
 QY 258 KVAVKNIK-CDVTAQAFLEDEFAVNTKKOHEMLVRLGLVILHGLIYVMEHVSKNLVNPL 316
 DB 311 RVAIKTLKPGTSPPEALQEAQVMKRLREKILVQLYAVVSEPIYIVLEWMSKGLNPL 370
 QY 317 PFRGRALVNTAQLLOFSLHVAEGMEYLESKRLVHRDLAARNILVSEDLVAKVSPGLAKA 376
 DB 371 KEMKGYLRLPDLVMAADIAAGMAYVEGMVYHNDLRAANILVGENLECKADGGLARL 430
 QY 377 ---ERKGLDSSRLPVWTAPALKHGFTSKSDVWSFGVLLMEVFSYGRADYPKMSLKE 432
 DB 431 IDNEEYTAQAGAKFPAKWTAPAGLYGRTITKSDVWSFGIILTELTKGRVYVPMGNCE 490
 QY 433 VSEAVENKGYRMEPECCPGPVHVLSSCMEAPARPPFRKLAERL 478
 DB 491 VLDREYRGYRMPCEPCESLHLMCOQWRREPRERPFTEYLQADL 536

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 Job time : 48 secs

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